

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 17, 2005, 00:09:32 ; Search time 169 Seconds
(without alignments)
1881.166 Million cell updates/sec

Title: US-10-645-546-2
Perfect score: 4.19
Sequence: 1 MSSWRHWPAMRLMGFCW.....IHTLLQNLAKASPYLDILG 822

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	4419	100.0	822	2	AAR81630 Human trk
2	4419	100.0	822	3	AAY51599 Human trk
3	4419	100.0	822	5	AAE27931 Human trk
4	4419	100.0	822	5	AAH50851 Human rec
5	4419	100.0	822	6	ABU56698 Lung canc
6	4419	100.0	822	7	ABR82949 Human trk
7	4419	100.0	822	7	ADAE4045 Human rec
8	4419	100.0	822	7	ADN39076 Cancer/an
9	4419	100.0	822	7	ADN39954 Cancer/an
10	4419	100.0	822	8	ADG92974 Neurotrop
11	4401	99.6	838	6	ABU56699 Lung canc
12	4401	99.6	838	7	ADN39078 Cancer/an
13	4223	95.6	847	2	AAW11941 GD, trkB f
14	4179.5	94.6	821	5	AAE27935 Mouse ful
15	4179.5	94.6	821	5	ABR82953 Mouse trk
16	4162.5	94.2	821	5	AAH50850 Rat recep
17	4162.5	94.2	821	5	AAE27933 Rat neura
18	2844	64.4	537	5	AAE27933 Human trk
19	2844	64.4	537	7	ABR82951 Human trk
20	2826	64.0	553	5	AAE27934 Human trk
21	2826	64.0	553	7	ABR82952 Human trk
22	2520	57.0	477	3	AAH51600 Human trk
23	2520	57.0	477	6	AAE27932 Human trk
24	2520	57.0	477	6	ABU56416 Lung canc
25	2520	57.0	477	7	ABR82950 Human ort

26	2520	57.0	477	7	ADN39955 Cancer/an
27	2520	57.0	477	7	ADN39953 Cancer/an
28	2520	57.0	477	8	ADN05038 Antipsori
29	2294	51.9	825	2	AAR81631 Human trk
30	2294	51.9	825	8	ABO84519 Human can
31	2294	51.9	825	8	ABO84516 Human can
32	2292.5	51.9	476	5	AAH15447 TK negati
33	2292.5	51.9	476	5	AAE27936 Mouse trk
34	2292.5	51.9	476	7	ABR82954 Mouse trk
35	2289	51.8	825	2	AAH06595 Neurotrop
36	2281.5	51.6	830	2	AAR81627 Human trk
37	2277	51.5	839	2	AAR81625 Human trk
38	2277	51.5	839	3	AAH51601 Human trk
39	2277	51.5	839	5	AAE27937 Human trk
40	2277	51.5	839	5	AAH50853 Human rec
41	2277	51.5	839	7	ABR82955 Human trk
42	2277	51.5	839	8	ABO84518 Human can
43	2276.5	51.5	850	2	AAW11942 GD, trkB f
44	2266.5	51.3	864	5	AAH50852 Rat recep
45	2259.5	51.1	808	5	AAH81284 Human trk

ALIGNMENTS

RESULT 1		AAR81630 standard; protein: 822 AA.	
ID	AAR81630	31-MAR-1996 (first entry)	
XX	AC	AAR81630;	
XX	DT	31-MAR-1996 (first entry)	
XX	XX	Human trkB receptor protein.	
XX	KW	trkB receptor; tyrosine-kinase; enzyme; protease; inflammation; pain;	
XX	KM	diagnosis; neurotrophic factor; kidney; lung; psychiatric disorder.	
XX	OS	Homo sapiens.	
XX	XX	Location/Qualifiers	
FT	Key	67.70	
FT	Misc-difference	/note= "potential N-linked glycosylation site"	
FT	FT	95.98	
FT	Misc-difference	/note= "potential N-linked glycosylation site"	
FT	FT	121.124	
FT	Misc-difference	/note= "potential N-linked glycosylation site"	
FT	FT	178.181	
FT	Misc-difference	/note= "potential N-linked glycosylation site"	
FT	FT	205.208	
FT	Misc-difference	/note= "potential N-linked glycosylation site"	
FT	FT	241.244	
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FT	FT	254.257	
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FT	FT	280.283	
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FT	FT	325.328	
FT	Misc-difference	/note= "potential N-linked glycosylation site"	
FT	FT	338.341	
FT	Misc-difference	/note= "potential N-linked glycosylation site"	
FT	FT	412.415	
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FT	FT	431.454	
FT	Domain	/note= "transmembrane domain"	
FT	FT	466	
FT	Misc-difference	/note= "splice site for truncated trkB"	
FT	FT	544.807	
FT	Domain	/note= "tyrosine-kinase domain"	
XX	XX	MO9525795-A1.	
XX	XX	28-SEP-1995.	

XX 17-MAR-1995; 95MO-US003426.
 XX 18-MAR-1994; 94US-00215139.
 PR 05-AUG-1994; 94US-00286846.
 PR 20-DEC-1994; 94US-00359705.
 XX (GETH) GENENTECH INC.
 PA Presta LG, Shelton DL, Urfer R;
 PI WPI: 1995-344616/44.
 XX N-PSDB; AAT00689.
 DR
 XX New human trkB and trkc poly-peptide(s) and fusion proteins contg. them -
 PT also DNA, vectors and transformed cells useful in treatment and diagnosis
 PT of abnormal neurotrophic factor expression, e.g. inflammatory pain.
 XX
 PS Claim 8; Fig 1A-B; 117bp; English.
 CC This sequence may be expressed recombinantly for the production of human
 CC trkB receptor, and to detect or amplify trkc genes. The encoded protein
 CC may be used as a reagent in kinase receptor activation assays, and
 CC therapeutically in diseases associated with over or under expression of
 CC neurotrophic factor (e.g. pain of inflammation, kidney, lung,
 CC cardiovascular or psychiatric disorders and some sorts of tumors). At
 CC the indicated splice site, AA 436-791 may be replaced by the sequence
 CC FVLFRKIPIDG (AAR81624)
 CC
 XX
 SQ Sequence 822 AA;

Query Match 100.0%; Score 4419; DB 2; Length 822;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSWIRHGGPAMRLKMGFCMLVVGFMRAAFACPTSCSCSARIMWCSPPSGIVAFPRLEP 60
 DB 1 MSSWIRHGGPAMRLKMGFCMLVVGFMRAAFACPTSCSCSARIMWCSPPSGIVAFPRLEP 60
 QY 61 NSVDPENITEIFIANQKRLIINEDDVEAYVGLNLTIVDSGLKFAVHAKAFKXSNLOHI 120
 DB 61 NSVDPENITEIFIANQKRLIINEDDVEAYVGLNLTIVDSGLKFAVHAKAFKXSNLOHI 120
 QY 121 NFRNKLITSLSRKHFRHLDSLILVGNPPTSCDIMWIKTLOBAKSSPTODLYCINES 180
 DB 121 NFRNKLITSLSRKHFRHLDSLILVGNPPTSCDIMWIKTLOBAKSSPTODLYCINES 180
 QY 181 SKNIPLANLOIPNGGLPSANLAAANLTVBEKSTITLCSVAGDPVPMYMDVGNLVSKM 240
 DB 181 SKNIPLANLOIPNGGLPSANLAAANLTVBEKSTITLCSVAGDPVPMYMDVGNLVSKM 240
 QY 241 NETSHTQGLRITNISDDSGKOISVABNLVGEDQSVMLTVFAFATITFLBSPSTDH 300
 DB 241 NETSHTQGLRITNISDDSGKOISVABNLVGEDQSVMLTVFAFATITFLBSPSTDH 300
 QY 301 WCIPFTVKNPKPALQWPFYNGAILNESKYICTKIHTVNTHTYHQCQLDNPTHMNGDYT 360
 DB 301 WCIPFTVKNPKPALQWPFYNGAILNESKYICTKIHTVNTHTYHQCQLDNPTHMNGDYT 360
 QY 361 LIANKEGKDEKQISAFPMGPGIDGAPNRYPVYIYEDGTANDIGDTTNSNEIPST 420
 DB 361 LIANKEGKDEKQISAFPMGPGIDGAPNRYPVYIYEDGTANDIGDTTNSNEIPST 420
 QY 421 DVTDKTRHLSYAVAVVIVSVGFCILVMLFLKLARHSFGKMGKSPASVYISNDDGASP 480
 DB 421 DVTDKTRHLSYAVAVVIVSVGFCILVMLFLKLARHSFGKMGKSPASVYISNDDGASP 480
 QY 481 LHHISNGSNTSSSGGPDVAVIIGTKIPVLENQYFGITNSQLKPDTPVOHIKRANIVL 540
 DB 481 LHHISNGSNTSSSGGPDVAVIIGTKIPVLENQYFGITNSQLKPDTPVOHIKRANIVL 540
 QY 541 KRELGGARFGKVFALACYNLCPEODKILVAVKTLKQASDNARKDFHREBELTNLOHEHI 600
 DB 541 KRELGGARFGKVFALACYNLCPEODKILVAVKTLKQASDNARKDFHREBELTNLOHEHI 600

DB 541 KRELGGARFGKVFALACYNLCPEODKILVAVKTLKQASDNARKDFHREBELTNLOHEHI 600
 QY 601 VKFYGVCSBGDPLIMVPEYMKHGDINKFLRAHPDPAVLAEGNPPTLTOSOMLHIAQOI 660
 DB 601 VKFYGVCSBGDPLIMVPEYMKHGDINKFLRAHPDPAVLAEGNPPTLTOSOMLHIAQOI 660
 QY 661 AAGMVTIASQHFVHRDLATNCLVGENLVKIDGFGMSRIVYSTDYRVGHTMLPIRMM 720
 DB 661 AAGMVTIASQHFVHRDLATNCLVGENLVKIDGFGMSRIVYSTDYRVGHTMLPIRMM 720
 QY 721 PPESIMTRKFTESDYSLSGVLMELFTYQKOPWYQLSNNVEICTQGRVLQRPRTCPQ 780
 DB 721 PPESIMTRKFTESDYSLSGVLMELFTYQKOPWYQLSNNVEICTQGRVLQRPRTCPQ 780
 QY 781 EYVELMGWQRPBHRKNIKGIHTLLQNLAKASPVYLDILG 822
 DB 781 EYVELMGWQRPBHRKNIKGIHTLLQNLAKASPVYLDILG 822

RESULT 2

AAV51599
 ID AAV51599 standard; protein; 822 AA.
 XX

AAV51599;

AC 30-MAY-2000 (first entry)

XX Human trkB receptor protein.

KM trkB; human; receptor tyrosine kinase; trkc; diagnosis; neurotrophin;

KW neurotrophic factor.

XX Homo sapiens.

PN US6027927-A.

PD 22-FEB-2000.

PF 01-OCT-1997; 97US-00942562.

XX 18-MAR-1994; 94US-00215139.

PR 05-AUG-1994; 94US-00286846.

PK 19-MAY-1995; 95US-00444597.

XX (GETH) GENENTECH INC.

PA Urfer R, Shelton DL, Presta LG;

PI WPI: 2000-194832/17.

DR N-PSDB; AAZ88839.

XX New human trk receptors useful in the diagnosis of various human

PT pathological conditions associated with elevated or reduced levels of

PT neurotrophins capable of binding trkB and/or trkc.

XX Claim 1; Col 63-68; 78pp; English.

PS This invention describes a novel isolated and purified polypeptide (I),

XX belonging to the trk family of receptor tyrosine kinases, trks and trkc.

CC (I) are useful in the purification of human neurotrophic factors and in

CC the diagnosis of various human pathological conditions associated with

CC elevated or reduced levels of neurotrophins capable of binding trkB

CC and/or trkc. This sequence represents the human trkb receptor described

XX in the method of the invention

SO Sequence 822 AA;

Query Match 100.0%; Score 4419; DB 3; Length 822;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSSWIRHGGPAMRLKMGFCMLVVGFMRAAFACPTSCSCSARIMWCSPPSGIVAFPRLEP 60
 DB 1 MSSWIRHGGPAMRLKMGFCMLVVGFMRAAFACPTSCSCSARIMWCSPPSGIVAFPRLEP 60

Db 1 MSSWIRHGMALMGFCMLVGFWRAPAFACPTSCKSASRIMCSPSPGIVAFPRLEP 60
 Qy 61 NSVDPENITTEIFIANOKRLEIINEDDVEAYVGLANLTIIVDSGLKFAHKAFLKXNSNIQHI 120
 Db 61 NSVDPENITTEIFIANOKRLEIINEDDVEAYVGLANLTIIVDSGLKFAHKAFLKXNSNIQHI 120
 Qy 121 NPTNKLTLSLRKAFRHLDELSELIVGNPFSCDIWIKTLQAKSPDPTQDLYCLANES 180
 Db 121 NPTNKLTLSLRKAFRHLDELSELIVGNPFSCDIWIKTLQAKSPDPTQDLYCLANES 180
 Qy 121 NPTNKLTLSLRKAFRHLDELSELIVGNPFSCDIWIKTLQAKSPDPTQDLYCLANES 180
 Db 121 NPTNKLTLSLRKAFRHLDELSELIVGNPFSCDIWIKTLQAKSPDPTQDLYCLANES 180
 Qy 181 SKNIPLANLOIPNCGLSANLAAPNLTVBEKSTITLSCSVAGDVPVPMYMDVGNLVSKM 240
 Db 181 SKNIPLANLOIPNCGLSANLAAPNLTVBEKSTITLSCSVAGDVPVPMYMDVGNLVSKM 240
 Qy 241 NETSHTQSLRITNIISSDDSGKQISCAVENLVGEDODSVNLTVHAPPTITLESPTSDDH 300
 Db 241 NETSHTQSLRITNIISSDDSGKQISCAVENLVGEDODSVNLTVHAPPTITLESPTSDDH 300
 Qy 301 WCIPFTYKGNPKPALQWFTNGAILNESKICTKIHVTNHTHYHGCLOLDNFTHMNGDYT 360
 Db 301 WCIPFTYKGNPKPALQWFTNGAILNESKICTKIHVTNHTHYHGCLOLDNFTHMNGDYT 360
 Qy 361 LIAKNEYGKDEKQISAHFMGPGIDGAPNYPVIVEDYGTANDIGDTTNRSEIPIST 420
 Db 361 LIAKNEYGKDEKQISAHFMGPGIDGAPNYPVIVEDYGTANDIGDTTNRSEIPIST 420
 Qy 421 DVTDKTGREHLSTVYAVVIVASVGFCLVLMFLKLARHSKFGKGPASVISNDSDASP 480
 Db 421 DVTDKTGREHLSTVYAVVIVASVGFCLVLMFLKLARHSKFGKGPASVISNDSDASP 480
 Qy 481 LIAHISNGSNTSSSEGGPDAVIGMTKIPVIEINPQYFGITNSOLKPDTFVQHIKRNITVL 540
 Db 481 LIAHISNGSNTSSSEGGPDAVIGMTKIPVIEINPQYFGITNSOLKPDTFVQHIKRNITVL 540
 Qy 541 KRELGEAGFGVFLAECYNLCPEODKILVAVKTLKQASDNARKOFHRAEALLTNLOHEHI 600
 Db 541 KRELGEAGFGVFLAECYNLCPEODKILVAVKTLKQASDNARKOFHRAEALLTNLOHEHI 600
 Qy 601 VKFPGVCVGEADPLMVFPEYMGHDKNFKFLRAHGPDAVIMARGNPTELTOGOMLHIAQOI 660
 Db 601 VKFPGVCVGEADPLMVFPEYMGHDKNFKFLRAHGPDAVIMARGNPTELTOGOMLHIAQOI 660
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 Db 661 AAGWVYLASQHFVRDLATRNCLVGENLVKIGDFGMSRDVYSTDYVVGSHMLPIKRM 720
 Qy 721 PPESIMTRKFTTESDVMISLVVLEIFTYGGKQPMYQOLSNNVEICTTGSRVLOPRTPCQ 780
 Db 721 PPESIMTRKFTTESDVMISLVVLEIFTYGGKQPMYQOLSNNVEICTTGSRVLOPRTPCQ 780
 Qy 781 EYVELMGQWQREPHMRKNIKGIHTLLONLAKASPVYDIIG 822
 Db 781 EYVELMGQWQREPHMRKNIKGIHTLLONLAKASPVYDIIG 822
 RESULT 3
 AAE27931
 ID AAE27931 standard; protein; 822 AA.
 AC AAE27931;
 AC AAE27931;
 DT 27-DEC-2002 (first entry)
 XX
 DE Human TrkB protein.
 XX Human; neurodegenerative disorder; neurodevelopmental disorder; TrkB;
 KM TrkB; Alzheimer's disease; AD; amyotrophic lateral sclerosis; ALS; PD;
 KM Parkinson's disease; Huntington's disease; HD; Lou Gehrig's disease;
 KM diabetic peripheral neuropathy; Down's syndrome; DS; neuroprotective;
 KM gene therapy; anticonvulsant; cerebroprotective; nootropic.
 XX Homo sapiens.
 OS
 XX

PN W0200267858-A2.
 XX 06-SEP-2002.
 XX 22-FEB-2002; 2002WO-US005151.
 PF 22-FEB-2001; 2001US-0270553P.
 XX (UYMA-) UNIV MARYLAND BALTIMORE.
 PA Krueger BK, Kingsbury TJ, Bambrick LL, Dorsey SG;
 PI WPI; 2002-698627/75.
 XX DR N-PSDB; AAD45786.
 XX
 PT Treating and/or preventing neurodegenerative and neurodevelopmental
 PT disorders such as Alzheimer's, Parkinson's and Huntington's diseases by
 PT altering the ratio of amount of full-length and truncated TrkB or TrkC
 PT polypeptides.
 PS Claim 47; Page 56-59; 96pp; English.
 XX
 CC The present invention relates to a method of treating neurodegenerative
 CC or neurodevelopmental disorders in a mammal which involves administering
 CC an isolated nucleic acid encoding a full-length TrkB or TrkC or their
 CC mutant, variant, homologue or fragment or an anti-sense RNA for truncated
 CC TrkB or TrkC isoforms, where they increase the amount of full-length TrkB
 CC or TrkC or decrease the amount of truncated TrkB or TrkC in treated
 CC neurons. The methods and compositions of the invention are useful for
 CC treating or preventing neurodegenerative or neurodevelopmental disorders
 CC such as Alzheimer's disease (AD), Parkinson's disease (PD), Huntington's
 CC disease (HD), amyotrophic lateral sclerosis (ALS), Lou Gehrig's disease,
 CC diabetic peripheral neuropathy, the adverse complications of Down's
 CC syndrome (DS) and other types of peripheral neuropathy. Sequences of the
 CC invention are also used in gene therapy. The present sequence is human
 CC TrkB protein
 CC
 SQ Sequence 822 AA;
 Query Match 100.0%; Score 4419; DB 5; Length 822;
 Best Local Similarity 100.0%; Prid. No. 0;
 Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MSSWIRHGMALMGFCMLVGFWRAPAFACPTSCKSASRIMCSPSPGIVAFPRLEP 60
 Db 1 MSSWIRHGMALMGFCMLVGFWRAPAFACPTSCKSASRIMCSPSPGIVAFPRLEP 60
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 Db 61 NSVDPENITTEIFIANOKRLEIINEDDVEAYVGLANLTIIVDSGLKFAHKAFLKXNSNIQHI 120
 Qy 121 NPTNKLTLSLRKAFRHLDELSELIVGNPFSCDIWIKTLQAKSPDPTQDLYCLANES 180
 Db 121 NPTNKLTLSLRKAFRHLDELSELIVGNPFSCDIWIKTLQAKSPDPTQDLYCLANES 180
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 Db 121 NPTNKLTLSLRKAFRHLDELSELIVGNPFSCDIWIKTLQAKSPDPTQDLYCLANES 180
 Qy 181 SKNIPLANLOIPNCGLSANLAAPNLTVBEKSTITLSCSVAGDVPVPMYMDVGNLVSKM 240
 Db 181 SKNIPLANLOIPNCGLSANLAAPNLTVBEKSTITLSCSVAGDVPVPMYMDVGNLVSKM 240
 Qy 241 NETSHTQSLRITNIISSDDSGKQISCAVENLVGEDODSVNLTVHAPPTITLESPTSDDH 300
 Db 241 NETSHTQSLRITNIISSDDSGKQISCAVENLVGEDODSVNLTVHAPPTITLESPTSDDH 300
 Qy 301 WCIPFTYKGNPKPALQWFTNGAILNESKICTKIHVTNHTHYHGCLOLDNFTHMNGDYT 360
 Db 301 WCIPFTYKGNPKPALQWFTNGAILNESKICTKIHVTNHTHYHGCLOLDNFTHMNGDYT 360
 Qy 361 LIAKNEYGKDEKQISAHFMGPGIDGAPNYPVIVEDYGTANDIGDTTNRSEIPIST 420
 Db 361 LIAKNEYGKDEKQISAHFMGPGIDGAPNYPVIVEDYGTANDIGDTTNRSEIPIST 420
 Qy 421 DVTDKTGREHLSTVYAVVIVASVGFCLVLMFLKLARHSKFGKGPASVISNDSDASP 480
 Db 421 DVTDKTGREHLSTVYAVVIVASVGFCLVLMFLKLARHSKFGKGPASVISNDSDASP 480

Db 421 DVTDKTGRHLVYAVVAVIASVGFCLLWMLFLIKLARHSKFGKGPASVYSNDDSGASP 480
 QY 481 LHHISNGSNTSSSEGGPDVAIIIGMTKIPVLENFQYGTNSQAKPDPFYQHIKRHNI VL 540
 Db 481 LHHISNGSNTSSSEGGPDVAIIIGMTKIPVLENFQYGTNSQAKPDPFYQHIKRHNI VL 540
 QY 541 KRELGEBAFGKVFIAECYNLCPEODKILVAVKTKDASDNARKDFHREAEILTNLOHEHI 600
 Db 541 KRELGEBAFGKVFIAECYNLCPEODKILVAVKTKDASDNARKDFHREAEILTNLOHEHI 600
 QY 601 VKFYGVCVEGDPPLIMVEFYMKHGDLNKEFLRAHGPDALMEAGNPPTLSTOSMLIAQOI 660
 Db 601 VKFYGVCVEGDPPLIMVEFYMKHGDLNKEFLRAHGPDALMEAGNPPTLSTOSMLIAQOI 660
 QY 661 AAGGVYLASQHPVARDLATRNCLVGENLVKIGDPGNSRDYSTDYRVGSHMLPIRM 720
 Db 661 AAGGVYLASQHPVARDLATRNCLVGENLVKIGDPGNSRDYSTDYRVGSHMLPIRM 720
 QY 721 PPBSIMRKTTTSDVMSLGVLTWEITTYGKQPYQLSNNEVIRCTQGRVLOKPRTCPO 780
 Db 721 PPBSIMRKTTTSDVMSLGVLTWEITTYGKQPYQLSNNEVIRCTQGRVLOKPRTCPO 780
 QY 781 EYVELMTCWOREPHMKNIKGIHTLLONAKASPVYLDILG 822
 Db 781 EYVELMTCWOREPHMKNIKGIHTLLONAKASPVYLDILG 822

RESULT 4

AAM50851
 ID AAM50851 standard; protein; 822 AA.

AC AAM50851;

DT 01-MAY-2002 (first entry)

XX Human receptor tyrosine kinase TrkB.

XX Receptor tyrosine kinase; TrkB; receptor; human;

KM brain derived growth factor; BDNF; neurotrophin-3; NT-3;

KM Huntington's disease; Parkinson's disease; Alzheimer's disease;

KM amyotrophic lateral sclerosis; neurodegenerative disease; cancer;

KM neuroprotective; neurotrophic; anticonvulsant; antiparkinsonian; enzyme;

KM cytoskeletal; therapy.

XX Homo sapiens.

OS

XX

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XX

XX

XX

XX

XX

Key Location/Qualifiers
 Peptide 1..31
 Protein /label= Signal_peptide
 Domain /label= Mature_protein
 Modified-site /label= Extracellular
 Domain /note= "N-glycosylated"
 Region /label= Leucine-rich_repeats
 Modified-site /note= "leucine-rich repeat 1"
 Region /note= "N-glycosylated"
 Modified-site /note= "leucine-rich repeat 2"
 Modified-site /note= "N-glycosylated"
 Modified-site /note= "N-glycosylated"
 Modified-site /note= "N-glycosylated"
 Modified-site /note= "N-glycosylated"
 Domain /note= "N-glycosylated"
 Modified-site /label= Ig-like_C2-type
 Modified-site /note= "N-glycosylated"

FT Modified-site 254
 FT /note= "N-glycosylated"
 FT Modified-site 280
 FT /note= "N-glycosylated"
 FT Domain 301..365
 FT /label= Ig-like_C2-type
 FT Modified-site 325
 FT /note= "N-glycosylated"
 FT Modified-site 338
 FT /note= "N-glycosylated"
 FT Modified-site 412
 FT /note= "N-glycosylated"
 FT Domain 431..454
 FT /label= Transmembrane
 FT Domain 455..822
 FT /label= Cytoplasmic
 FT Misc-difference 467..477
 FT /note= "replaced by FULFKRIPLDG is truncated isoform"
 FT Misc-difference 478..822
 FT /note= "missing in truncated isoform"
 FT Binding-site 516
 FT /note= "interaction with SHC protein"
 FT Modified-site 516
 FT /note= "O-phosphorylated"
 FT Domain 538..807
 FT /label= Protein_kinase
 FT Region 544..552
 FT /note= "ATP binding site"
 FT Region 572
 FT /note= "ATP binding site"
 FT Active-site 676
 FT Modified-site 702
 FT /note= "O-phosphorylated"
 FT Modified-site 706
 FT /note= "O-phosphorylated"
 FT Modified-site 707
 FT /note= "O-phosphorylated"
 FT Binding-site 817
 FT /note= "interaction with PLC-gamma-1"
 FT Modified-site 817
 FT /note= "O-phosphorylated"

XX WC200203071-A2.

XX 10-JAN-2002.

XX 05-JUL-2001, 2001MO-US021472.

XX 05-JUL-2000, 2000US-0215778P.

XX (PANG-) PANGENE CORP.

XX Bates AT;

XX WPI, 2002-179638/23.

XX Screening for a neurotrophic factor mimetic, useful for treating, e.g.,

XX cancer and Alzheimer's, comprises combining a candidate mimetic with a

XX fragment of a tyrosine kinase protein.

XX Disclosure; Fig 11A; 107pp; English.

XX The present sequence is that of human receptor tyrosine kinase TrkB, the

XX receptor for brain-derived growth factor (BDNF) and neurotrophin-3 (NT-

XX 3). The invention concerns Trks and their ligands that modulate cell

XX growth, differentiation and survival. Trk proteins are known to mediate

XX the activities of neurotrophins and are also known proto-oncogenes.

XX Methods are claimed for screening for small molecule neurotrophic factor

XX (NTP) mimetics, such as the cyclic peptide given in AAM50844, capable of

XX binding to a Trk protein or of modulating the binding of a neurotrophin

XX to a Trk protein. Also claimed are medicaments comprising a small

XX molecule NTP mimetic and their use in claimed methods for treatment of

XX cancer or a neurodegenerative disease selected from Huntington's disease,

CC Parkinson's disease, Alzheimer's disease and amyotrophic lateral sclerosis
 CC
 XX
 XX

Sequence 822 AA;

Query Match 100.0%; Score 4419; DB 5; Length 822;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSWIRHGPAMALMGFCMLVGVFWRAAFACPTSCCKSASRIMCSDPSPGIVAFPRLEP 60
 DB 1 MSSWIRHGPAMALMGFCMLVGVFWRAAFACPTSCCKSASRIMCSDPSPGIVAFPRLEP 60
 QY 61 NSVDPENITEIFIANOKRLIINEDDVEAYVGLNLTIVDSGLKFAVHAKAFKXSNLOHI 120
 DB 61 NSVDPENITEIFIANOKRLIINEDDVEAYVGLNLTIVDSGLKFAVHAKAFKXSNLOHI 120
 QY 121 NPTNKLTSLSRKAFRHLDSELLVGNPFTCSDIMIKTLQBAKSSPTQDLYCLNES 180
 DB 121 NPTNKLTSLSRKAFRHLDSELLVGNPFTCSDIMIKTLQBAKSSPTQDLYCLNES 180
 QY 181 SKNPLANLOIPNCGLPANLAAPNLTEBEGKSITLSCVAGDPVPMNYMDVGNLVSKM 240
 DB 181 SKNPLANLOIPNCGLPANLAAPNLTEBEGKSITLSCVAGDPVPMNYMDVGNLVSKM 240
 QY 241 NETSHTQSLRITNISSDSGKOISCVANLVGEDSDSVNLTVHAPPTITLESPTSDEH 300
 DB 241 NETSHTQSLRITNISSDSGKOISCVANLVGEDSDSVNLTVHAPPTITLESPTSDEH 300
 QY 301 WCIPFTVGNKPKPALQWFTNGAILNESKYICTKIHVTNHTYHGCLOLDNPTMANNQDYT 360
 DB 301 WCIPFTVGNKPKPALQWFTNGAILNESKYICTKIHVTNHTYHGCLOLDNPTMANNQDYT 360
 QY 361 LIAKNEYKDKKOISAHFMWPGIDGPNRYPRVIYDYCTAANDIGDTNRSNEIPST 420
 DB 361 LIAKNEYKDKKOISAHFMWPGIDGPNRYPRVIYDYCTAANDIGDTNRSNEIPST 420
 QY 421 DVDTKTGREHLSYAVVVIASVGFCLVLMFLKLARHSFKMGKGPASVISNDDSDASP 480
 DB 421 DVDTKTGREHLSYAVVVIASVGFCLVLMFLKLARHSFKMGKGPASVISNDDSDASP 480
 QY 481 LHHISNSGNTSPSSBEGPDVAVIGMTKIPVIEENPOYFGITNSOLKPDTFVOHKKRHNIVL 540
 DB 481 LHHISNSGNTSPSSBEGPDVAVIGMTKIPVIEENPOYFGITNSOLKPDTFVOHKKRHNIVL 540
 QY 541 KRELGEAFGKVFPLAECYNLCPEODKILVAVKTLKDSADNARKDFHRAEALLTNLOHHEI 600
 DB 541 KRELGEAFGKVFPLAECYNLCPEODKILVAVKTLKDSADNARKDFHRAEALLTNLOHHEI 600
 QY 601 VKFYGVCSBGPDLIMVFEMHGDINKFLRAHGPDAVLMAGNPPTTELTOGOMLHIAQOI 660
 DB 601 VKFYGVCSBGPDLIMVFEMHGDINKFLRAHGPDAVLMAGNPPTTELTOGOMLHIAQOI 660
 QY 661 AAGWVYLASQHFVARDLATRNCLVGENLVKIGDFGMSRDYSTDYRVVGHITMLPIKMM 720
 DB 661 AAGWVYLASQHFVARDLATRNCLVGENLVKIGDFGMSRDYSTDYRVVGHITMLPIKMM 720
 QY 721 PPBSIMTRKFTTESDWSLGVVLWEIFTYGQPMYQOLSNNEVICTITGRLVQRPRTCPQ 780
 DB 721 PPBSIMTRKFTTESDWSLGVVLWEIFTYGQPMYQOLSNNEVICTITGRLVQRPRTCPQ 780
 QY 781 EYVELMLGCWQREPMRNKINGIHTLONLAKASPVYLDIIG 822
 DB 781 EYVELMLGCWQREPMRNKINGIHTLONLAKASPVYLDIIG 822

RESULT 5
 ID ABUS6698 standard; protein; 822 AA.
 AC ABUS6698;
 XX

DT 02-APR-2003 (first entry)

XX Lung cancer-associated polypeptide #291.
 DE
 XX
 XX
 KW Lung cancer-associated polypeptide; cytosolic; emphysema;
 KW antiinflammatory; antisthmatic; non-small cell lung cancer; atelectasis;
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
 XX
 OS Unidentified.
 XX
 XX
 PN W0200286443-A2.
 PD
 PD 31-OCT-2002.
 PF 18-APR-2002; 2002MO-US012476.
 XX
 XX 18-APR-2001; 2001US-0284770P.
 PR 10-MAY-2001; 2001US-0290492P.
 PR 09-NOV-2001; 2001US-0339245P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 29-NOV-2001; 2001US-0334370P.
 PR 12-APR-2002; 2002US-0372246P.
 XX
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 XX Aziz N, Murray R;
 PI WPI, 2003-093161/08.
 DR N-PSDB; ABX76427.
 DR
 XX
 PT Detecting a lung cancer-associated transcript in a cell from a patient
 PT for treating lung cancer, by contacting a biological sample from the
 PT patient with a polynucleotide that exhibits increased or decreased
 PT expression in lung cancer.
 PS Claim 27; Page 417-418; 453pp; English.
 XX
 XX The invention relates to a method for detecting a lung cancer-associated
 CC transcript in a cell from a patient, comprising contacting a biological
 CC sample from the patient with a polynucleotide that selectively hybridises
 CC to a sequence that is at least 80 % identical to a gene that exhibits
 CC increased or decreased expression in lung cancer samples. Lung cancer-
 CC associated polynucleotides and polypeptides are used for identifying a
 CC compound that modulates a lung cancer-associated polypeptide, for
 CC inhibiting proliferation of a lung cancer-associated cell to treat lung
 CC cancer in a patient and for treating a mammal having lung cancer by
 CC administering a modulatory compound identified. The methods are useful
 CC for treating lung cancer, such as small cell lung cancer, non-small cell
 CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
 CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
 CC hyperresponsivity pneumonitis, interstitial pulmonary fibrosis, asthma and
 CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
 CC for diagnostic purposes and as targets for screening for therapeutic
 CC compounds that modulate lung cancer, such as antibodies. Sequences
 CC ABUS6698-ABUS6745 represent lung cancer-associated polypeptides of the
 CC invention
 CC
 XX
 XX
 SQ Sequence 822 AA;
 Query Match 100.0%; Score 4419; DB 6; Length 822;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSSWIRHGPAMALMGFCMLVGVFWRAAFACPTSCCKSASRIMCSDPSPGIVAFPRLEP 60
 DB 1 MSSWIRHGPAMALMGFCMLVGVFWRAAFACPTSCCKSASRIMCSDPSPGIVAFPRLEP 60
 QY 61 NSVDPENITEIFIANOKRLIINEDDVEAYVGLNLTIVDSGLKFAVHAKAFKXSNLOHI 120
 DB 61 NSVDPENITEIFIANOKRLIINEDDVEAYVGLNLTIVDSGLKFAVHAKAFKXSNLOHI 120
 QY 121 NPTNKLTSLSRKAFRHLDSELLVGNPFTCSDIMIKTLQBAKSSPTQDLYCLNES 180

```

Db      121 NFRNKLTSLSRGRFRLDLSELILVGNPFTCSDDIMMITLQBAKSSPTQDLYCLNES 180
Qy      181 SKNIPLANLOIPNCGPSANLAAPNLTVBEGKSITLSCSVAQDPVPMYDVGNLVSKM 240
Db      181 SKNIPLANLOIPNCGPSANLAAPNLTVBEGKSITLSCSVAQDPVPMYDVGNLVSKM 240
Qy      241 NETSHTQGSRLRTNISSDSGSKQISCAVENLVGEDQDSVNLTVFAPTITFLSPISDHH 300
Db      241 NETSHTQGSRLRTNISSDSGSKQISCAVENLVGEDQDSVNLTVFAPTITFLSPISDHH 300
Qy      301 WCIPFTYKGNPKPALQMFYNGALINBSKYICTKIHVTNHTBHGCLQDNPPTMNNQDYT 360
Db      301 WCIPFTYKGNPKPALQMFYNGALINBSKYICTKIHVTNHTBHGCLQDNPPTMNNQDYT 360
Qy      361 LIANNEYGKDEKQISAHFMGPGIDGAPNYPDVITYEDYGTANDIGDTTNSNEIPST 420
Db      361 LIANNEYGKDEKQISAHFMGPGIDGAPNYPDVITYEDYGTANDIGDTTNSNEIPST 420
Qy      421 DVTDKTGREHLASYAAVVVIVASVGFCLVNLFLKLARSHKFGMKGPASVISNDDBASP 480
Db      421 DVTDKTGREHLASYAAVVVIVASVGFCLVNLFLKLARSHKFGMKGPASVISNDDBASP 480
Qy      481 LHHISNGSNTSSSEGGPDVAITIGMTKIPVLENPOYFGITNSQKPDPTFOHIKRHHIVL 540
Db      481 LHHISNGSNTSSSEGGPDVAITIGMTKIPVLENPOYFGITNSQKPDPTFOHIKRHHIVL 540
Qy      541 KRELISGAPGKVFALBECYNLCPEODKILIVAVTKLDASDNARKDPRHREASLITNLQHEHI 600
Db      541 KRELISGAPGKVFALBECYNLCPEODKILIVAVTKLDASDNARKDPRHREASLITNLQHEHI 600
Qy      601 VKFPGVCBEGDPLIMVEBEMKRGDLAKFLRAHGDAVLMAEGNPTELTOGOMLHIAQOI 660
Db      601 VKFPGVCBEGDPLIMVEBEMKRGDLAKFLRAHGDAVLMAEGNPTELTOGOMLHIAQOI 660
Qy      661 AAGGVVYASQHFVARDLATRNCVLGENILVYKIDFGMSRDYSDYYRVGGHTMLPIRRM 720
Db      661 AAGGVVYASQHFVARDLATRNCVLGENILVYKIDFGMSRDYSDYYRVGGHTMLPIRRM 720
Qy      721 PPSISIMRKFTTESDVMSLGVLMELFTYQKQPMYQOLSNNVEIEICITQGRVLQRPRTCPQ 780
Db      721 PPSISIMRKFTTESDVMSLGVLMELFTYQKQPMYQOLSNNVEIEICITQGRVLQRPRTCPQ 780
Qy      781 EYVELMIGCWOREBPMKRNKIKGHTLLQNLAKASPVYLDILG 822
Db      781 EYVELMIGCWOREBPMKRNKIKGHTLLQNLAKASPVYLDILG 822

RESULT 6
ABR82949 standard; protein; 822 AA.
XX      ABR82949;
XX      18-DEC-2003 (first entry)
XX      Human TrkB polypeptide.
XX      TrkB; TrkC; neurodegenerative; neuro-developmental; antiparkinsonian;
XX      neuroprotective; anticonvulsant; cerebroprotective; vasotropic;
XX      nocotropic; human.
XX      Homo sapiens.
XX      OS
XX      PN      WO2003071872-A1.
XX      PD      04-SEP-2003.
XX      XX      28-MAY-2002; 2002WO-US016807.
XX      PF      22-FEB-2002; 2002WO-US005151.
XX      PR      (UTMA-) UNIV MARYLAND BALTIMORE.
XX      PA

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PA      (KRUE/) KRUEGER B K.
PA      (KING/) KINGSBURY T J.
PA      (BAMB/) BAMBRICK L L.
PA      (DORS/) DORSEY S G.
XX
PI      Krueger BK, Kingsbury TJ, Bambrick LL, Dorsey SG;
XX
XX      WPI, 2003-731549/69.
XX      DR      N-PSDB; ACF36565.
XX
PT      Treating and/or preventing neurodegenerative or neuro-developmental
PT      disorders, such as Alzheimer's disease, Parkinson's disease and
PT      amyotrophic lateral sclerosis, using nucleic acids encoding TrkB and/or
PT      TrkC polypeptides.
XX
XX      Claim 47; Page 58-61; 99pp; English.
XX
CC      The invention relates to treating a neurodegenerative or neuro-
CC      developmental disorder in a mammal. The method involves altering the
CC      ratio of the amount of full length TrkB polypeptide to the amount of
CC      truncated TrkB polypeptides in a neuron or by altering the ratio of the
CC      amount of full length TrkC polypeptide to the amount of truncated TrkC
CC      polypeptides in a neuron. The methods and compositions of the present
CC      invention are useful for treating and/or preventing a neurodegenerative
CC      or neuro-developmental disorder, such as Alzheimer's disease, Parkinson's
CC      disease, Huntington's disease, amyotrophic lateral sclerosis (Lou
CC      Gehrig's disease), the adverse neurologic complications of Down syndrome,
CC      diabetic peripheral neuropathy and other types of peripheral neuropathy,
CC      and is associated with an injury to the central or peripheral nervous
CC      system resulting from stroke, cerebral ischaemia, or chemical and/or
CC      physical trauma. The present sequence represents a human TrkB polypeptide
CC      (Genbank Accession No. NM_006180)
XX
SQ      Sequence 822 AA:
XX
Query Match      100.0%; Score 4419; DB 7; Length 822;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy      1 MSSMIRHNGPAMRLNGFCMLVVGFMRAAFACPTSCKSASRIWCSDPSPGIVAFPLRP 60
Db      1 MSSMIRHNGPAMRLNGFCMLVVGFMRAAFACPTSCKSASRIWCSDPSPGIVAFPLRP 60
Qy      61 NSVDPENITEIFIANQRLIEINEDVEAYVGRNLITVDSGLKFAVAKAFKNSNIQHT 120
Db      61 NSVDPENITEIFIANQRLIEINEDVEAYVGRNLITVDSGLKFAVAKAFKNSNIQHT 120
Qy      121 NFRNKLTSLSRGRFRLDLSELILVGNPFTCSDDIMMITLQBAKSSPTQDLYCLNES 180
Db      121 NFRNKLTSLSRGRFRLDLSELILVGNPFTCSDDIMMITLQBAKSSPTQDLYCLNES 180
Qy      181 SKNIPLANLOIPNCGPSANLAAPNLTVBEGKSITLSCSVAQDPVPMYDVGNLVSKM 240
Db      181 SKNIPLANLOIPNCGPSANLAAPNLTVBEGKSITLSCSVAQDPVPMYDVGNLVSKM 240
Qy      241 NETSHTQGSRLRTNISSDSGSKQISCAVENLVGEDQDSVNLTVFAPTITFLSPISDHH 300
Db      241 NETSHTQGSRLRTNISSDSGSKQISCAVENLVGEDQDSVNLTVFAPTITFLSPISDHH 300
Qy      301 WCIPFTYKGNPKPALQMFYNGALINBSKYICTKIHVTNHTBHGCLQDNPPTMNNQDYT 360
Db      301 WCIPFTYKGNPKPALQMFYNGALINBSKYICTKIHVTNHTBHGCLQDNPPTMNNQDYT 360
Qy      361 LIANNEYGKDEKQISAHFMGPGIDGAPNYPDVITYEDYGTANDIGDTTNSNEIPST 420
Db      361 LIANNEYGKDEKQISAHFMGPGIDGAPNYPDVITYEDYGTANDIGDTTNSNEIPST 420
Qy      421 DVTDKTGREHLASYAAVVVIVASVGFCLVNLFLKLARSHKFGMKGPASVISNDDBASP 480
Db      421 DVTDKTGREHLASYAAVVVIVASVGFCLVNLFLKLARSHKFGMKGPASVISNDDBASP 480
Qy      481 LHHISNGSNTSSSEGGPDVAITIGMTKIPVLENPOYFGITNSQKPDPTFOHIKRHHIVL 540
Db      481 LHHISNGSNTSSSEGGPDVAITIGMTKIPVLENPOYFGITNSQKPDPTFOHIKRHHIVL 540

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Db 481 LHHISNGSNTPSSSEGGPDVAIIIGMTKIPVLENPOYFGITNSQLKPDPTFVOHIKRHNIIVL 540
 Qy 541 KRELGEBAFGKVFPLAECYNLCPEODKILVAVKTKLSDASDNARKDFHREAEILLTNLOHEHI 600
 Db 541 KRELGEBAFGKVFPLAECYNLCPEODKILVAVKTKLSDASDNARKDFHREAEILLTNLOHEHI 600
 Qy 601 VKFYGVCEGDPILIMVEFYMKHGDINKFLRAHGPDAVLMAGNPTELTQSOMLHIAQOI 660
 Db 601 VKFYGVCEGDPILIMVEFYMKHGDINKFLRAHGPDAVLMAGNPTELTQSOMLHIAQOI 660
 Qy 661 AAGNVYLASQHFVHRDLATRNCLVGENILVKIGDFGMSRDVSYDYRVGHTMLPIRMM 720
 Db 661 AAGNVYLASQHFVHRDLATRNCLVGENILVKIGDFGMSRDVSYDYRVGHTMLPIRMM 720
 Qy 721 PPESIMRKFTTESDVMISGLVLMWEIFTYGKQPMYQLSNNEVICITQGRVLOPRPTCPQ 780
 Db 721 PPESIMRKFTTESDVMISGLVLMWEIFTYGKQPMYQLSNNEVICITQGRVLOPRPTCPQ 780
 Qy 781 EYVELMIGCWQREPHMRKNIKIGITLLQNLAKASPVYIDLIG 822
 Db 781 EYVELMIGCWQREPHMRKNIKIGITLLQNLAKASPVYIDLIG 822

RESULT 7 ADE40445

ID ADE40445 standard; protein; 822 AA.

AC ADE40445;

DT 29-JAN-2004 (first entry)

DE Human receptor tyrosine kinase TRKB (gene ID 5816) protein.

XX AIDS; acquired immunodeficiency syndrome; human immunodeficiency virus;
 KM HIV-related disorder; differential expression; drug screening;
 KM viral replication modulation; diagnosis; prognosis; predisposition;
 KM anti-HIV; gene therapy; antisense therapy; human;
 XX receptor tyrosine kinase TRKB; enzyme.
 KM Homo sapiens.
 OS W02003070883-A2.
 PN 28-AUG-2003.
 PD 13-FEB-2003; 2003WO-US004246.
 XX 15-FEB-2002; 2002US-0357391P.
 XX 13-MAY-2002; 2002US-0380249P.
 XX 25-JUN-2002; 2002US-0391306P.
 XX 27-AUG-2002; 2002US-0406297P.
 XX 19-SEP-2002; 2002US-0412007P.
 XX 10-OCT-2002; 2002US-0417508P.
 XX 10-DEC-2002; 2002US-0432318P.
 XX (MILL-) MILLENNIUM PHARM INC.
 PA
 PI Powell DM, Weich NS;
 XX WPI; 2003-671808/63.
 DR N-PSDB; ADE40444.
 XX

PT Identifying a compound capable of diagnosing, preventing or treating AIDS
 PT or an HIV-related disorder comprises assaying the ability of the compound
 PT to modulate e.g. 1414, 1481 or 1553 nucleic acid expression or
 PT polypeptide activity.
 XX Claim 1; SEQ ID NO 24; 167bp; English.
 PS
 CC The invention relates to a method of identifying a compound useful in the
 CC treatment of AIDS (acquired immunodeficiency syndrome) or an HIV (human
 CC immunodeficiency virus)-related disorder. The invention involves assaying
 CC the ability of a test compound to modulate the activity or expression of

CC 26 human proteins. These proteins and nucleic acids encoding them
 CC (ADE40422-ADE40473) are differentially expressed in tissues relating to
 CC AIDS or an HIV-related disorder compared to their expression in normal
 CC tissues. The invention also relates to the use of the compounds
 CC identified to modulate viral replication in a cell and to treat a patient
 CC with AIDS or an HIV-related disorder. The invention further discloses
 CC methods for the diagnostic evaluation and prognosis of various HIV-
 CC related disorders, and for the identification of individuals exhibiting a
 CC predisposition to such conditions. The modulatory compounds identified
 CC using the method of the invention may be small organic molecules,
 CC peptides, antibodies or antisense nucleic acid molecules. The methods of
 CC the invention are useful in diagnosing, preventing or treating AIDS or
 CC HIV-related disorders. The present sequence represents a human protein
 CC which is differentially expressed in AIDS or HIV-related disorders.
 CC
 XX
 SQ Sequence 822 AA;

Query Match 100.0%; Score 4419; DB 7; Length 822;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSSWIRHGPAMARLWGCMLVGFWRAPACPTSCKSASRIWCSPPSGIVAPRRLEP 60
 Db 1 MSSWIRHGPAMARLWGCMLVGFWRAPACPTSCKSASRIWCSPPSGIVAPRRLEP 60
 Qy 61 NSVDPENITTEIFIANOKRELIINEDVEAYVGNLTITVDSGLRFVAHAKFLKSNLQHI 120
 Db 61 NSVDPENITTEIFIANOKRELIINEDVEAYVGNLTITVDSGLRFVAHAKFLKSNLQHI 120
 Qy 121 NFRNKLTSLSRKAFRHLDELILVGNPPTSCDINWIKTLQEAKSSPTDYLCLNES 180
 Db 121 NFRNKLTSLSRKAFRHLDELILVGNPPTSCDINWIKTLQEAKSSPTDYLCLNES 180
 Qy 181 SKNIPLANLOIPNGCLGSANLAAENLVREBSKLTLSCSVAGDPVPMYVGNLVSGM 240
 Db 181 SKNIPLANLOIPNGCLGSANLAAENLVREBSKLTLSCSVAGDPVPMYVGNLVSGM 240
 Qy 241 NETSHTQSLRITNITSSDDSGKOISVAENLVGBDQSVNLTVAFAPTITLESPTSDDH 300
 Db 241 NETSHTQSLRITNITSSDDSGKOISVAENLVGBDQSVNLTVAFAPTITLESPTSDDH 300
 Qy 241 NETSHTQSLRITNITSSDDSGKOISVAENLVGBDQSVNLTVAFAPTITLESPTSDDH 300
 Db 241 NETSHTQSLRITNITSSDDSGKOISVAENLVGBDQSVNLTVAFAPTITLESPTSDDH 300
 Qy 301 WCIPFTVKNPKPALQWPNYNGAILNESKYICTKIHTVNTHEYHCLQIDNPTHMNGDYT 360
 Db 301 WCIPFTVKNPKPALQWPNYNGAILNESKYICTKIHTVNTHEYHCLQIDNPTHMNGDYT 360
 Qy 361 LIAKNEYGKDEKQISAFPMGPGIDGDANPNYPVIVYEDYGTANDIGDTNRSNEIPST 420
 Db 361 LIAKNEYGKDEKQISAFPMGPGIDGDANPNYPVIVYEDYGTANDIGDTNRSNEIPST 420
 Qy 421 DVTDKTGBHLSYAAVVVIVASVGFCLVLMFLKLRHSFKGKGPASVTSNDDDSASP 480
 Db 421 DVTDKTGBHLSYAAVVVIVASVGFCLVLMFLKLRHSFKGKGPASVTSNDDDSASP 480
 Qy 481 LHHISNGSNTPSSSEGGPDVAIIIGMTKIPVLENPOYFGITNSQLKPDPTFVOHIKRHNIIVL 540
 Db 481 LHHISNGSNTPSSSEGGPDVAIIIGMTKIPVLENPOYFGITNSQLKPDPTFVOHIKRHNIIVL 540
 Qy 541 KRELGEBAFGKVFPLAECYNLCPEODKILVAVKTKLSDASDNARKDFHREAEILLTNLOHEHI 600
 Db 541 KRELGEBAFGKVFPLAECYNLCPEODKILVAVKTKLSDASDNARKDFHREAEILLTNLOHEHI 600
 Qy 601 VKFYGVCEGDPILIMVEFYMKHGDINKFLRAHGPDAVLMAGNPTELTQSOMLHIAQOI 660
 Db 601 VKFYGVCEGDPILIMVEFYMKHGDINKFLRAHGPDAVLMAGNPTELTQSOMLHIAQOI 660
 Qy 661 AAGNVYLASQHFVHRDLATRNCLVGENILVKIGDFGMSRDVSYDYRVGHTMLPIRMM 720
 Db 661 AAGNVYLASQHFVHRDLATRNCLVGENILVKIGDFGMSRDVSYDYRVGHTMLPIRMM 720
 Qy 721 PPESIMRKFTTESDVMISGLVLMWEIFTYGKQPMYQLSNNEVICITQGRVLOPRPTCPQ 780
 Db 721 PPESIMRKFTTESDVMISGLVLMWEIFTYGKQPMYQLSNNEVICITQGRVLOPRPTCPQ 780

QY 781 EVELMLGCMQREBPHMRKNIKGIHTLLQNLAKASPVYLDILG 822
Db 781 EVELMLGCMQREBPHMRKNIKGIHTLLQNLAKASPVYLDILG 822

RESULT 8
ADN39076 ID ADN39076 standard; protein, 822 AA.

XX ADN39076;
XX 17-JUN-2004 (first entry)
XX
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:394.

XX Human, differential expression; cancer; angiogenic disorder;
KM fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KM inflammatory disease; autoimmune disease;
KM retinal neovascularisation syndrome; scarring; uterine fibroid;
KM detection; diagnosis; prognosis; drug screening; drug targeting;
KM wound healing; contraception; cytostatic; cardiac; immunomodulatory;
KM vulnery; gene therapy; vaccine.

XX Homo sapiens.
OS
PN M02003042661-A2.
PD 22-MAY-2003.
PF 13-NOV-2002; 2002MO-US036610.

XX 13-NOV-2001; 2001US-0350666P.
PR 21-NOV-2001; 2001US-0332464P.
PR 29-NOV-2001; 2001US-0334393P.
PR 03-DEC-2001; 2001US-0335394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-0355250P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-0368099P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.
PR 16-JUN-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-0397775P.
PR 22-JUL-2002; 2002US-0397845P.
PR 09-SEP-2002; 2002US-0409450P.

XX (BOSB-) BOS BIOTECHNOLOGY INC.
PA
PI Afeef D, Aziz N, Gansburg WM, Gish KC, Glynn R, Hevezzi PA;
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnick A;
XX
XX WPI; 2003-468649/44.
DR N-PSDB; ADN39075.

XX Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.
PT
XX
PS Claim 12; SEQ ID NO 394; 1385DP; English.

XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide at least 80% identical to
CC the invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;

CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularisation syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a polypeptide of the invention.
XX
XX Sequence 822 AA;
SQ
Query Match 100.0%; Score 4419; DB 7; Length 822;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSWIRHGMARLWGMFCWLVGFWRAFAACPTSCCKSARWCSPPQIVAFPLRP 60
Db 1 MSSWIRHGMARLWGMFCWLVGFWRAFAACPTSCCKSARWCSPPQIVAFPLRP 60

QY 61 NSVDPENITFIPLANQRLAIINEDVBAVYGLRNLTIYVSGLKFVAHKAFLKNSNIQHI 120
Db 61 NSVDPENITFIPLANQRLAIINEDVBAVYGLRNLTIYVSGLKFVAHKAFLKNSNIQHI 120

QY 121 NPTRNKLTLSRKHFRHLDSEILVGNPFTSCDIMWITKLOAKSPPTODLYCLNES 180
Db 121 NPTRNKLTLSRKHFRHLDSEILVGNPFTSCDIMWITKLOAKSPPTODLYCLNES 180

QY 181 SKNIPLANLQIPNCGLPISANLAAPNLVEBKGKSTTSCSAVADPVPMMYDVGNLVSKM 240
Db 181 SKNIPLANLQIPNCGLPISANLAAPNLVEBKGKSTTSCSAVADPVPMMYDVGNLVSKM 240

QY 241 NETSHTQSLRITNISSDDSGKQISCAENLVGHDQDSVNLTVFAPTTIFLESPTSDH 300
Db 241 NETSHTQSLRITNISSDDSGKQISCAENLVGHDQDSVNLTVFAPTTIFLESPTSDH 300

QY 301 WCIPFTYKGNPKPALQFNYGALINBSKYCTKHVNHTEBYGCLQDNPPTHMNGDYT 360
Db 301 WCIPFTYKGNPKPALQFNYGALINBSKYCTKHVNHTEBYGCLQDNPPTHMNGDYT 360

QY 361 LIANBYGKDEKQISAFPMWPGIDGANDPNYPVIEYEDYTAANDIGDTTNSNEIPST 420
Db 361 LIANBYGKDEKQISAFPMWPGIDGANDPNYPVIEYEDYTAANDIGDTTNSNEIPST 420

QY 421 DVTDKTGRHLSTYAAVVVYASVVGFCLLVNLFLIKLARHSKFGMKGPASVYSNDDDSASP 480
Db 421 DVTDKTGRHLSTYAAVVVYASVVGFCLLVNLFLIKLARHSKFGMKGPASVYSNDDDSASP 480

QY 481 LHHISNGSNTPSSSEGGPDVITIGMTKIPVIEHQYFGITNSOLKPTPFQHIRHNVIL 540
Db 481 LHHISNGSNTPSSSEGGPDVITIGMTKIPVIEHQYFGITNSOLKPTPFQHIRHNVIL 540

QY 541 KRELGEAGFGKVFALACYNLCPEBODKILVAVKTLKADSDNARKDFHREBELTLQHEHI 600
Db 541 KRELGEAGFGKVFALACYNLCPEBODKILVAVKTLKADSDNARKDFHREBELTLQHEHI 600

QY 601 VKFYGVCEBDDPLIMVEBYMKHGDINKFLRAHGPDAVLAEGNPPTBLTOSQMLHIAQOI 660
Db 601 VKFYGVCEBDDPLIMVEBYMKHGDINKFLRAHGPDAVLAEGNPPTBLTOSQMLHIAQOI 660

QY 661 AAGGVYLASQHPVHRDLATNCLVGENLVLYKIDPFGMSRPVYSIDYRVGHTMLPIRMM 720
Db 661 AAGGVYLASQHPVHRDLATNCLVGENLVLYKIDPFGMSRPVYSIDYRVGHTMLPIRMM 720

QY 721 PPESIMYRKFTTESDVVSLGVLMIEITTYGKQPPYQOLSNNBEVICTQGRVLOPRPCPO 780
Db 721 PPESIMYRKFTTESDVVSLGVLMIEITTYGKQPPYQOLSNNBEVICTQGRVLOPRPCPO 780

QY 781 EVELMLGCMQREBPHMRKNIKGIHTLLQNLAKASPVYLDILG 822
Db 781 EVELMLGCMQREBPHMRKNIKGIHTLLQNLAKASPVYLDILG 822

RESULT 9

ADN39954
ID ADN39954 standard; protein; 822 AA.
XX
AC ADN39954;
XX
DT 17-JUN-2004 (first entry)
XX
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C324.
XX
KM Human; differential expression; cancer; angiogenic disorder;
KM fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KM inflammatory disease; autoimmune disease;
KM retinal neovascularization syndrome; scarring; uterine fibroid;
KM detection; diagnosis; prognosis; drug screening; drug targeting;
KM wound healing; contraception; cytostatic; cardiac; immunomodulatory;
KM vulnery; gene therapy; vaccine.
XX
OS Homo sapiens.
PN W02003042661-A2.
PD 22-MAY-2003.
PF 13-NOV-2002; 2002WO-US036810.
XX
PR 13-NOV-2001; 2001US-0350666P.
PR 21-NOV-2001; 2001US-0332464P.
PR 29-NOV-2001; 2001US-0334393P.
PR 03-DEC-2001; 2001US-0335394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-0355250P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-0368809P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.
PR 16-JUL-2002; 2002US-0386838P.
PR 22-JUL-2002; 2002US-0397775P.
PR 22-JUL-2002; 2002US-0397845P.
PR 09-SEP-2002; 2002US-0409450P.
XX
PA (BOSB-) BOS BIOTECHNOLOGY INC.
XX
PI Afer D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Heyezi PA;
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX
DR WPI: 2003-468649/44.
DR N-PSDB: ADN39737.
XX
PT Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
XX a nucleic acid in a biological sample.
XX
PS Claim 12; SEQ ID NO C324; 1385bp; English.
XX
XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularization syndromes, scarring and uterine fibroids. They may

CC also be useful in wound healing and in contraception. The present
CC sequence represents a polypeptide of the invention.
XX
SQ Sequence 822 AA;
Query Match 100.0%; Score 4419; DB 7; Length 822;
Best local similarity 100.0%; Pred. No. 0;
Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSSWIRHGPAMALMGFCMLVGFMPRAAPCPPTSCCKSARICSPDPSRIVAPRRP 60
DB 1 MSSWIRHGPAMALMGFCMLVGFMPRAAPCPPTSCCKSARICSPDPSRIVAPRRP 60
QY 61 NSVDPENITETIFIANQRLBINEEDVEAYVGLNLTIVSGLFVFAHKAFLKSNLOHI 120
DB 61 NSVDPENITETIFIANQRLBINEEDVEAYVGLNLTIVBSGLFVFAHKAFLKSNLOHI 120
QY 121 NFRNKLTSLSRKHFRHLDSEILVGNPPTGCDIMWIKTLQBAKSSPTQDLYCLNES 180
DB 121 NFRNKLTSLSRKHFRHLDSEILVGNPPTGCDIMWIKTLQBAKSSPTQDLYCLNES 180
QY 181 SKNIPLANLQIPNGLPSANLAPNLTVBEGKSTTSCSVAGDPVPMYMDVGNLVSGHM 240
DB 181 SKNIPLANLQIPNGLPSANLAPNLTVBEGKSTTSCSVAGDPVPMYMDVGNLVSGHM 240
QY 241 NETSTQSLRITNYSDDSGKOISCAENLVGEDDVSMLTVFAPTITLESPTSDDH 300
DB 241 NETSTQSLRITNYSDDSGKOISCAENLVGEDDVSMLTVFAPTITLESPTSDDH 300
QY 301 WCIPFTVGNPKPALQWFGNALINESKYICTKHVTNTHREYHCLQDNPTHMNGDYT 360
DB 301 WCIPFTVGNPKPALQWFGNALINESKYICTKHVTNTHREYHCLQDNPTHMNGDYT 360
QY 361 LIANNEYGKOBKQISAFPMGPGIDGAPNYPVYIYEDYTAANDIGDTNRSNEIPST 420
DB 361 LIANNEYGKOBKQISAFPMGPGIDGAPNYPVYIYEDYTAANDIGDTNRSNEIPST 420
QY 421 DVIDKTRERHLYAVAVVIVASVGFCLVLMFLIKLARHSFGKGPASVISNDDDSASP 480
DB 421 DVIDKTRERHLYAVAVVIVASVGFCLVLMFLIKLARHSFGKGPASVISNDDDSASP 480
QY 481 LHHISNGSNTPPSSSEGGPDVAITGMTKIPVLENPOYEGITNSQLKPTFVQHIRHNVL 540
DB 481 LHHISNGSNTPPSSSEGGPDVAITGMTKIPVLENPOYEGITNSQLKPTFVQHIRHNVL 540
QY 541 KREIAGEGAFGVFLAECYNLCPEQDKILVAVKTLKSDASDARKDPFHREAEELITNLQHEHI 600
DB 541 KREIAGEGAFGVFLAECYNLCPEQDKILVAVKTLKSDASDARKDPFHREAEELITNLQHEHI 600
QY 601 VKFYGVCEBDPLIMVEFEMKGGDLNKEFLRAHGDAVILMEGNPTELTOGMLHIAQOI 660
DB 601 VKFYGVCEBDPLIMVEFEMKGGDLNKEFLRAHGDAVILMEGNPTELTOGMLHIAQOI 660
QY 661 AAGWVYLASQHFVARDLATRNCVGENLVKIGFGKSRDYSIDYIRVGHNTMLPIRM 720
DB 661 AAGWVYLASQHFVARDLATRNCVGENLVKIGFGKSRDYSIDYIRVGHNTMLPIRM 720
QY 721 PPESIMYRKFTTESDVSLSGVIMEIFTYGKOPYQLSNNEVICITQGRVLRPRCPQ 780
DB 721 PPESIMYRKFTTESDVSLSGVIMEIFTYGKOPYQLSNNEVICITQGRVLRPRCPQ 780
QY 781 EYVELMLGCMQREPHMKNIKIGHTLLQNLAKASPVYLDILG 822
DB 781 EYVELMLGCMQREPHMKNIKIGHTLLQNLAKASPVYLDILG 822
RESULT 10
ID ADS92974 standard; protein; 822 AA.
XX
AC ADS92974;
XX
DT 02-DEC-2004 (first entry)

XX Neurotrophic tyrosine kinase receptor type 2.
 XX cytostatic; gene therapy; human;
 KM branching morphogenesis modulating agent; MBM agent.
 XX Homo sapiens.
 OS
 FN W02004037990-A2.
 PD 06-MAY-2004.
 PF 22-OCT-2003; 2003WO-US033549.
 PR 23-OCT-2002; 2002US-0420554P.
 PR 30-DEC-2002; 2002US-0436941P.
 PA (EXEL-) EXELIXIS INC.
 PI Plowman GD, Karim FD, Swimer C, Habeck HA, Koblipek TI;
 PI Schulte-Werker S, Langheinrich U, Stott GM, Trowe T, Vogel AM;
 PI Odenthal JH, Scheel JK, Will TT, Jin Y, Berke LM, Hai B;
 PI Adamkiewicz JJ, Lickteig K, Hammonds RGR, Amundsen CD, Zhang H;
 PI Nicoll M;
 XX WPI; 2004-365506/34.
 DR N-PSDB; ADS92943.
 PT Identifying a candidate branching morphogenesis modulating agent for
 PT treating cancer comprises contacting the assay system comprising a MBM
 PT polypeptide or nucleic acid with a test agent and detecting a test agent-
 PT biased activity.
 XX
 XX Example 3; SEQ ID NO 45; 179pp; English.
 XX
 CC The invention describes a method of identifying a candidate branching
 CC morphogenesis modulating (MBM) agent. The method comprises: providing an
 CC assay system comprising a MBM polypeptide or nucleic acid; contacting the
 CC assay system with a test agent under conditions where the system provides
 CC a reference activity, except for the presence of the test agent; and
 CC detecting a test agent-biased activity of the assay system, where a
 CC difference between the test agent-biased activity and the reference
 CC activity identifies the test agent as a candidate branching morphogenesis
 CC modulating agent. Also described are: a method of modulating branching
 CC morphogenesis in a mammalian cell; and a method for diagnosing a disease
 CC in a patient. The method is useful in identifying a candidate branching
 CC morphogenesis modulating agent for preparing a composition for diagnosing
 CC or treating cancer. This is the amino acid sequence of a human branching
 CC morphogenesis modulating (MBM) protein.
 CC
 XX
 XX Sequence 822 AA;
 SQ
 Query Match 100.0%; Score 4419; DB 8; Length 822;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 241 NETSHQSLRITNINSSDSDSGKOISCVAENLVGDDQSVNLTVHAPPTIFLESPTSDH 300
 QY 301 WCIPFTYKGNPKPALOMFYNGAILNBSKYICTKHVTNHTHYGCIQLDNPTHMNGDYT 360
 DB 301 WCIPFTYKGNPKPALOMFYNGAILNBSKYICTKHVTNHTHYGCIQLDNPTHMNGDYT 360
 QY 361 LIAKNEYGDEKQISAHPFMWPGIDGAPNPYVDVYEDYGTANDIGDTTNSNEIPST 420
 DB 361 LIAKNEYGDEKQISAHPFMWPGIDGAPNPYVDVYEDYGTANDIGDTTNSNEIPST 420
 QY 421 DVTDKTGREHLSTYAAVVVIVASVGFCLVNLFLTKLARSHKFGMKGPASVYSNDDDSASP 480
 DB 421 DVTDKTGREHLSTYAAVVVIVASVGFCLVNLFLTKLARSHKFGMKGPASVYSNDDDSASP 480
 QY 481 LHHISNGSNTSSSEGGPDVVIIGMTKIPYIENPOYFGITNSQLKPDTPVOHIKRHHIVL 540
 DB 481 LHHISNGSNTSSSEGGPDVVIIGMTKIPYIENPOYFGITNSQLKPDTPVOHIKRHHIVL 540
 QY 541 KRELGGAGFGKVTLAECYNI CPEODKILVAVKTLKASDARXODFHRBAELTNLOHEHI 600
 DB 541 KRELGGAGFGKVTLAECYNI CPEODKILVAVKTLKASDARXODFHRBAELTNLOHEHI 600
 QY 601 VKFYGVCVBGDPILMVFEYMKHGDNLKFLRAHGPDAVLMAEGNPTELTQSOMLHTAQOI 660
 DB 601 VKFYGVCVBGDPILMVFEYMKHGDNLKFLRAHGPDAVLMAEGNPTELTQSOMLHTAQOI 660
 QY 661 AAGWVYLASQHFHRDLATNCLVGENLVKIGDPGMSRDVYSTDYRVGHTMLPIRM 720
 DB 661 AAGWVYLASQHFHRDLATNCLVGENLVKIGDPGMSRDVYSTDYRVGHTMLPIRM 720
 QY 721 PPSIMYRKRTTSDVWSLGVIMETTYGKOPYQLSNNEVEICTIQGVLOPRPCPO 780
 DB 721 PPSIMYRKRTTSDVWSLGVIMETTYGKOPYQLSNNEVEICTIQGVLOPRPCPO 780
 QY 781 EYVELMIGCQOREPHMKNIKGIHTLLQNLAKSPVYLDILG 822
 DB 781 EYVELMIGCQOREPHMKNIKGIHTLLQNLAKSPVYLDILG 822

RESULT 11
 ID ABUS6699 standard; protein; 838 AA.
 XX
 XX ABUS6699;
 AC
 XX 02-Apr-2003 (first entry)
 DT
 XX
 DE Lung cancer-associated polypeptide #292.
 XX
 XX Lung cancer-associated polypeptide; cytostatic; emphysema;
 KM antiinflammatory; antileastmatic; non-small cell lung cancer; atelectasis;
 KM small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KM chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KM interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
 XX
 OS unidentified.
 XX
 FN W0200286443-A2.
 PD 31-OCT-2002.
 PF 18-Apr-2002; 2002WO-US012476.
 PR 18-Apr-2001; 2001US-0284770P.
 PR 10-MAY-2001; 2001US-0290492P.
 PR 09-NOV-2001; 2001US-0359245P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 29-NOV-2001; 2001US-0334370P.
 PR 12-Apr-2002; 2002US-0372246P.
 XX
 PA (BOSB-) BOS BIOTECHNOLOGY INC.

PI Aziz N, Murray R;
XX WPI; 2003-093161/08.
DR N-PSDB; ABX76428.
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.
XX
PS Claim 27; Page 418-419; 453pp; English.
XX
CC The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung cancer-
CC associated polynucleotides and polypeptides are used for identifying a
CC compound that modulates a lung cancer-associated polypeptide, for
CC inhibiting proliferation of a lung cancer-associated cell to treat lung
CC cancer in a patient and for treating a mammal having lung cancer by
CC administering a modulatory compound identified. The methods are useful
CC for treating lung cancer, such as small cell lung cancer, non-small cell
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hyperaerability pneumonia, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the
CC invention
XX
SQ Sequence 838 AA;
XX
Query Match 99.6%; Score 4401; DB 6; Length 838;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 822; Conservative 0; Mismatches 0; Indels 16; Gaps 1;
XX
QY 1 MSSWIRHGMAMLMGFCWLVGFWRAPACPTSCCKSARICSPSPGIVAFPRLEP 60
Db 1 MSSWIRHGMAMLMGFCWLVGFWRAPACPTSCCKSARICSPSPGIVAFPRLEP 60
XX
QY 61 NSVDPENITTEIFIANOKRLIELINEDVEAYVGLNLTIVDSGLKFAVAKAFKASNLQHI 120
Db 61 NSVDPENITTEIFIANOKRLIELINEDVEAYVGLNLTIVDSGLKFAVAKAFKASNLQHI 120
XX
QY 121 NFRNKLTSLSRKFRHLIDSELILVGNPFTSCDIIWIKTLQBAKSSPTDYLCLNES 180
Db 121 NFRNKLTSLSRKFRHLIDSELILVGNPFTSCDIIWIKTLQBAKSSPTDYLCLNES 180
XX
QY 181 SKNIPLANLOIPNCGLPBANLAAPULYVEBKSTITSCSVAQDVPVPMYVGMVLVSKM 240
Db 181 SKNIPLANLOIPNCGLPBANLAAPULYVEBKSTITSCSVAQDVPVPMYVGMVLVSKM 240
XX
QY 241 NETSHTOGSLRITNISDDSGKOISCAVENLVGEDDQSVNLTVFAPPTITLESPTQJHH 300
Db 241 NETSHTOGSLRITNISDDSGKOISCAVENLVGEDDQSVNLTVFAPPTITLESPTQJHH 300
XX
QY 301 WCIPFYKGNKPAALQWPFYNGAILNESKYICTKIHTNHTYHGCLOLDNPTNANGDYT 360
Db 301 WCIPFYKGNKPAALQWPFYNGAILNESKYICTKIHTNHTYHGCLOLDNPTNANGDYT 360
XX
QY 361 LIAKNEYGKQKQISAFHFMWPGIDGAPNPYPIVYEDYGTANDIGDTTNRSENEIPST 420
Db 361 LIAKNEYGKQKQISAFHFMWPGIDGAPNPYPIVYEDYGTANDIGDTTNRSENEIPST 420
XX
QY 421 DVTDKTGRHLVAVVVIASVGFCLLVMFLFKLARSHKFGKMK----- 465
Db 421 DVTDKTGRHLVAVVVIASVGFCLLVMFLFKLARSHKFGKMKPSWFGVKYSRQG 480
XX
QY 466 -GPASVISNDDDSAPLHHISNGSNTBSSSGGPDAVIIGWTKI PVLENPOYFGITNSQL 524
Db 466 -GPASVISNDDDSAPLHHISNGSNTBSSSGGPDAVIIGWTKI PVLENPOYFGITNSQL 524
XX
QY 481 VGPASVISNDDDSAPLHHISNGSNTBSSSGGPDAVIIGWTKI PVLENPOYFGITNSQL 540
Db 481 VGPASVISNDDDSAPLHHISNGSNTBSSSGGPDAVIIGWTKI PVLENPOYFGITNSQL 540

QY 525 KPDTFVQHIRKHNIVLKRLEBEGAFGKVFPLAECYNLCPEODKILVAVKTLKASDNARKD 584
Db 541 KPDTFVQHIRKHNIVLKRLEBEGAFGKVFPLAECYNLCPEODKILVAVKTLKASDNARKD 600
XX
QY 585 FHRBAELLTLQHEHIYKFPVCYEGDPLIMVBYMKHGDLNKLRAHGPDVILMAEGNP 644
Db 601 FHRBAELLTLQHEHIYKFPVCYEGDPLIMVBYMKHGDLNKLRAHGPDVILMAEGNP 660
XX
QY 645 PTELTSQMLHIAQOILAGWVYLASQHFVRDLATRNCLVGENLVLVIGFGMSRDVYST 704
Db 661 PTELTSQMLHIAQOILAGWVYLASQHFVRDLATRNCLVGENLVLVIGFGMSRDVYST 720
XX
QY 705 DYRVGSHMLPIRMMPBESIMYRKFTTESDWSLGVLMIEFTYGKQWYQLSNNEVIE 764
Db 721 DYRVGSHMLPIRMMPBESIMYRKFTTESDWSLGVLMIEFTYGKQWYQLSNNEVIE 780
XX
QY 765 CITQGRVLRPRPCQGVVEYELMGQWRBPMRNKINIGITLLQNLAKASPVYLDIIG 822
Db 781 CITQGRVLRPRPCQGVVEYELMGQWRBPMRNKINIGITLLQNLAKASPVYLDIIG 838
XX
RESULT 12
ADN39078
ID ADN39078 standard; protein; 838 AA.
XX
AC ADN39078;
XX
DT 17-JUN-2004 (first entry)
XX
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:396.
XX
KW Human: differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW rectinal neovascularisation syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiac; immunomodulatory;
KW vulnereary; gene therapy; vaccine.
XX
OS Homo sapiens.
PN W02003042661-A2.
XX
PD 22-MAY-2003.
XX
PE 13-NOV-2002; 2002WC-US036810.
XX
PR 13-NOV-2001; 2001US-0350666P.
PR 21-NOV-2001; 2001US-0332464P.
PR 29-NOV-2001; 2001US-0334383P.
PR 03-DEC-2001; 2001US-0335394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-047211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-035250P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-0368809P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.
PR 16-JUL-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-0397775P.
PR 22-JUL-2002; 2002US-0397845P.
PR 09-SEP-2002; 2002US-0409450P.
XX
PA (E0SB-) BOS BIOTECHNOLOGY INC.
XX
FI Afer D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnick A;
XX WPI; 2003-468649/44.

QY 181 SKNPLANLQIPNCGIPSAANLAAPNLTVBERGKSTITLSCSVAAGDPVPMYVGNLVSKM 240
 DB 181 SKNPLANLQIPNCGIPSAANLAAPNLTVBERGKSTITLSCSVAAGDPVPMYVGNLVSKM 240
 QY 241 NETSHTOGSLRITNISDDSGKOISCAVENLVGEDQSVNLTVFAFATITFLBESPTSDH 300
 DB 241 NETSHTOGSLRITNISDDSGKOISCAVENLVGEDQSVNLTVFAFATITFLBESPTSDH 300
 QY 301 WCIPFTYKGNPKPALQWFFYNGAILNESKYICTKIHVTNHTBYHGCQLDNPPTMANGDYT 360
 DB 301 WCIPFTYKGNPKPALQWFFYNGAILNESKYICTKIHVTNHTBYHGCQLDNPPTMANGDYT 360
 QY 361 LIANNEYGKDEKQISAHFMGPGIDGAPNYPVPIVEDYGTANDIGDTTNKSNELPST 420
 DB 361 LIANNEYGKDEKQISAHFMGPGIDGAPNYPVPIVEDYGTANDIGDTTNKSNELPST 420
 QY 421 DVTDKTGRHLASYAVAVVIVASVGFCLLVMLFLKLARHSKFGKGPASVISNDDDSASP 480
 DB 421 DVTDKTGRHLASYAVAVVIVASVGFCLLVMLFLKLARHSKFGKGPASVISNDDDSASP 480
 QY 481 LHHISNGSNTPPSSSEGGPDVAITIGMTKIPVIENTPOYFGITNSOLKPDTPVOHIGRHNIVL 540
 DB 481 LHHISNGSNTPPSSSEGGPDVAITIGMTKIPVIENTPOYFGITNSOLKPDTPVOHIGRHNIVL 540
 QY 541 KREIBGAPGVFLAECYNLCPEODKILVANKTKDASDNARKDPHREABLLTNLQHEHI 600
 DB 541 KREIBGAPGVFLAECYNLCPEODKILVANKTKDASDNARKDPHREABLLTNLQHEHI 600
 QY 601 VKFPGVCVEGDPILMVEFYMGGDLNKFRAHGPDAVLMAGNPPTTELTSOMLHIAQOI 660
 DB 601 VKFPGVCVEGDPILMVEFYMGGDLNKFRAHGPDAVLMAGNPPTTELTSOMLHIAQOI 660
 QY 661 AAGAVYIASQHFVARDIATNRCVGENLVKIGDFGMSRDVYSTDYRVGGHTMLPIRMM 720
 DB 661 AAGAVYIASQHFVARDIATNRCVGENLVKIGDFGMSRDVYSTDYRVGGHTMLPIRMM 720
 QY 721 PPBSIMRKFTTESDWSLGVVLMETFTYQKQPMYQOLSNNEVICITQGRVLQRPRTCPQ 780
 DB 721 PPBSIMRKFTTESDWSLGVVLMETFTYQKQPMYQOLSNNEVICITQGRVLQRPRTCPQ 780
 QY 781 EYVELMIGCMQREPHMRKINIGITLONLAKASPVYLDILG 822
 DB 781 EYVELMIGCMQREPHMRKINIGITLONLAKASPVYLDILG 822

RESULT 15
 ABR82953 ID ABR82953 standard; protein; 821 AA.
 AC ABR82953;
 DT 18-DEC-2003 (first entry)
 DE Mouse TrkB polypeptide.
 KM TrkB; TrkC; neurodegenerative; neuro-developmental; antiparkinsonian;
 KM neuroprotective; anticonvulsant; cerebroprotective; vasotropic;
 OS nootropic; mouse.
 OS Mus musculus.
 XX MO2003071872-A1.
 PD 04-SEP-2003.
 PF 28-MAY-2002; 2002MO-US016807.
 PR 22-FEB-2002; 2002MO-US005151.
 XX (UTMA-) UNIV MARYLAND BALTIMORE.
 PA (KRUE/) KRUEGER B K.
 PA (KING/) KINGSBURY T J.
 PA (BAMB/) BAMBRICK L U.

PA (DORSEY/) DORSEY S G.
 XX Krueger BK, Kingsbury TJ, Bambrick LL, Dorsey SG;
 PI WPI; 2003-731549/69.
 DR N-PSDB; ACF36569.
 XX
 PT Treating and/or preventing neurodegenerative or neuro-developmental
 PT disorders, such as Alzheimer's disease, Parkinson's disease and
 PT amyotrophic lateral sclerosis, using nucleic acids encoding trkB and/or
 PT TrkB polypeptides.
 XX
 PS Claim 48; Page 80-83; 99pp; English.
 XX
 CC The invention relates to treating a neurodegenerative or neuro-
 CC developmental disorder in a mammal. The method involves altering the
 CC ratio of the amount of full length TrkB polypeptide to the amount of
 CC truncated TrkB polypeptides in a neuron or by altering the ratio of the
 CC amount of full length TrkB polypeptide to the amount of truncated TrkB
 CC polypeptides in a neuron. The methods and compositions of the present
 CC invention are useful for treating and/or preventing a neurodegenerative
 CC or neuro-developmental disorder, such as Alzheimer's disease, Parkinson's
 CC disease, Huntington's disease, amyotrophic lateral sclerosis (Lou
 CC Gehrig's disease), the adverse neurologic complications of Down syndrome,
 CC diabetic peripheral neuropathy and other types of peripheral neuropathy,
 CC and is associated with an injury to the central or peripheral nervous
 CC system resulting from stroke, cerebral ischaemia, or chemical and/or
 CC physical trauma. The present sequence represents a mouse TrkB polypeptide
 CC (GenBank Accession No. X17647)
 XX
 SQ Sequence 821 AA.
 Query Match 94.6%; Score 4179.5; DB 7; Length 821;
 Best Local Similarity 93.9%; Pred. No. 0;
 Matches 772; Conservative 27; Mismatches 22; Indels 1; Gaps 1;
 QY 1 MSWIRKRGAMARLWGFCLLVGFMRAAFACPTSCSCSARIMCSDPSGIVAFPLRP 60
 DB 1 MSWIRKRGAMARLWGFCLLVGFMRAAFACPTSCSCSARIMCSDPSGIVAFPLRP 60
 QY 61 NSVDPENITIFIANQGRLEINBDVDEAVYVGNLTIVYSGLFVYHKAFLKSNINQHI 120
 DB 61 NSVDPENITIFIANQGRLEINBDVDEAVYVGNLTIVYSGLFVYHKAFLKSNINQHI 120
 QY 121 NFRNKLTLSRKHFRHLDSEILVGNPPTSCDIIWIKILOEAKSPPTODLYCINES 180
 DB 121 NFRNKLTLSRKHFRHLDSEILVGNPPTSCDIIWIKILOEAKSPPTODLYCINES 180
 QY 181 SKNPLANLQIPNCGIPSAANLAAPNLTVBERGKSTITLSCSVAAGDPVPMYVGNLVSKM 240
 DB 181 SKNPLANLQIPNCGIPSAANLAAPNLTVBERGKSTITLSCSVAAGDPVPMYVGNLVSKM 240
 QY 241 NETSHTOGSLRITNISDDSGKOISCAVENLVGEDQSVNLTVFAFATITFLBESPTSDH 300
 DB 241 NETSHTOGSLRITNISDDSGKOISCAVENLVGEDQSVNLTVFAFATITFLBESPTSDH 300
 QY 301 WCIPFTYKGNPKPALQWFFYNGAILNESKYICTKIHVTNHTBYHGCQLDNPPTMANGDYT 360
 DB 301 WCIPFTYKGNPKPALQWFFYNGAILNESKYICTKIHVTNHTBYHGCQLDNPPTMANGDYT 360
 QY 361 LIANNEYGKDEKQISAHFMGPGIDGAPNYPVPIVEDYGTANDIGDTTNKSNELPST 420
 DB 361 LIANNEYGKDEKQISAHFMGPGIDGAPNYPVPIVEDYGTANDIGDTTNKSNELPST 420
 QY 421 DVTDKTGRHLASYAVAVVIVASVGFCLLVMLFLKLARHSKFGKGPASVISNDDDSASP 480
 DB 421 DVTDKTGRHLASYAVAVVIVASVGFCLLVMLFLKLARHSKFGKGPASVISNDDDSASP 480
 QY 481 LHHISNGSNTPPSSSEGGPDVAITIGMTKIPVIENTPOYFGITNSOLKPDTPVOHIGRHNIVL 540
 DB 481 LHHISNGSNTPPSSSEGGPDVAITIGMTKIPVIENTPOYFGITNSOLKPDTPVOHIGRHNIVL 540
 QY 541 KREIBGAPGVFLAECYNLCPEODKILVANKTKDASDNARKDPHREABLLTNLQHEHI 600

Db	540	KRELGEAFGKVFPLACYNLCPEODKILVAVKTLKDASDNARKDFHREABELLTNIQHEHI	599
Qy	601	VKPYGVCVEGDPPLIMVFEMGHGDLINKFLRAHGPDAVIMAEGNPPTELTOSOMLHIAQOI	660
Db	600	VKPYGVCVEGDPPLIMVFEMGHGDLINKFLRAHGPDAVIMAEGNPPTELTOSOMLHIAQOI	659
Qy	661	AAGNVYLASQHFVHRDLATRNCVGENLLVKIGDFGMSRDVYSTDYRVGHTMLPIRM	720
Db	660	AAGNVYLASQHFVHRDLATRNCVGENLLVKIGDFGMSRDVYSTDYRVGHTMLPIRM	719
Qy	721	PPESIMYRKFTTESDWSLGIVVWEIFTYKQOPWYQLSNNEVIBCTTQGRVLORRPTCPQ	780
Db	720	PPESIMYRKFTTESDWSLGIVVWEIFTYKQOPWYQLSNNEVIBCTTQGRVLORRPTCPQ	779
Qy	781	EVEIEMLGQWOBPPMRKNIGIHITLQNLAKASPVYIDILG	822
Db	780	EVEIEMLGQWOBPPMRKNIGIHITLQNLAKASPVYIDILG	821

Search completed: February 17, 2005, 00:24:24
 Job time : 174 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 17, 2005, 00:10:23 ; Search time 178 Seconds
(without alignments)
2364.770 Million cell updates/sec

Title: US-10-645-546-2
Perfect score: 4419
Sequence: 1 MSSMIRWHPMARLMGFCW.....IHTLLQNIKAKSPVYDILG 822

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4419	100.0	822	1 TRKB_HUMAN	Q16620 homo sapien
2	4401	99.6	838	2 O8WKJ7	O8WKJ7 homo sapien
3	4179.5	94.6	821	1 TRKB_MOUSE	P15209 mus musculu
4	4162.5	94.2	821	1 TRKB_RAT	O63604 rattus norv
5	3426	77.5	818	1 TRKB_CHICK	Q91987 gallus gall
6	3091.5	70.0	821	2 Q9YH44	Q9YH44 xenopus lae
7	3078.5	69.7	811	2 Q9YH43	Q9YH43 xenopus lae
8	2896.5	65.5	669	2 O6B515	O6B515 poephila gu
9	2826	64.0	553	2 O8WKJ5	O8WKJ5 homo sapien
10	2296	52.0	825	2 O6VNS1	O6VNS1 mus musculu
11	2282.5	51.9	476	2 O8OWU0	O8OWU0 mus musculu
12	2277	51.5	839	1 TRKB_HUMAN	Q16288 homo sapien
13	2277	51.5	839	2 O75682	O75682 homo sapien
14	2275	51.5	827	1 TRKB_CHICK	O91044 gallus gall
15	2266.5	51.3	864	1 TRKB_RAT	O03351 rattus norv
16	2178	49.3	825	1 TRKB_PIG	P24786 sus scrofa
17	2107	47.7	486	2 Q9PST9	Q9PST9 xenopus lae
18	1943.5	44.0	790	2 Q90699	Q90699 gallus gall
19	1916.5	43.4	778	1 TRKA_CHICK	Q91009 gallus gall
20	1901.5	43.0	796	1 TRKA_HUMAN	P04629 homo sapien
21	1901	43.0	799	1 TRKA_RAT	P36739 rattus norv
22	1430.5	32.1	282	2 Q91373	Q91373 xenopus. tr
23	1263.5	28.6	476	2 Q7ZXJ8	Q7ZXJ8 xenopus lae
24	1249	28.3	503	2 Q15655	Q15655 homo sapien
25	1098.5	24.9	794	1 TRK1_LYMSST	O76997 lymnaea sca
26	991	22.4	612	2 Q922P9	Q922P9 lymnaea sca
27	989	22.4	612	2 Q96CV4	Q96CV4 homo sapien
28	969	21.9	185	2 Q9GMA1	Q9GMA1 cercopithec
29	858.5	19.4	868	1 MUSK_RAT	O62838 rattus norv
30	854	19.3	869	1 MUSK_HUMAN	O5146 homo sapien
31	850.5	19.2	868	1 MUSK_MOUSE	O61006 mus musculu

32	844.5	19.1	1145	2 Q9BK18	Q9BK18 alysiata cal
33	798	18.1	946	2 Q07153	Q07153 torpedo cal
34	789.5	17.9	947	1 MUSK_CHICK	O6AXY6 gallus gall
35	763.5	17.3	502	2 Q9Z200	Q9Z200 mus musculu
36	757	17.1	626	2 Q7OIP0	Q7OIP0 anopheles g
37	749	16.9	685	1 ROR1_DROME	Q24488 drosophila
38	736	16.7	553	2 Q7Z2S2	Q7Z2S2 brachydanio
39	734	16.6	354	2 Q9DDA2	Q9DDA2 xenopus lae
40	731	16.5	863	2 Q7Q5T3	Q7Q5T3 anopheles g
41	722	16.3	937	1 ROR1_HUMAN	O01973 homo sapien
42	720	16.3	896	2 Q7Q5C2	Q7Q5C2 gallus gall
43	717.5	16.2	724	1 ROR2_DROME	Q96K3 drosophila
44	716	16.2	178	2 Q95K65	Q95K65 macaca fasc
45	716	16.2	948	2 Q9Y1Y6	Q9Y1Y6 ephydactia f

ALIGNMENTS

RESULT 1
TRKB_HUMAN STANDARD; PRT; 822 AA.
ID: TRKB_HUMAN
AC Q16620; Q16675; O8WKJ6;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE BDNF/NT-3 growth factors receptor precursor (BC 2.7.1.112) (TrkB
DE tyrosine kinase) (GPI45-T-KB) (Trk-B).
GN Name=NTK2; Synonyms=TRKB;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Metazoa; Primates; Catarrhini; Homiidae; Homo.
NX NCBI_Taxid=9606;
[1]
[1] SEQUENCE FROM N.A. (ISOFORM TRKB).
RP TISSUE=Hippocampus;
RX MEDLINE=95309922; PubMed=7789988;
RA Nakagawara A., Liu X.-G., Ikegaki N., White P.S., Yamashiro D.J.,
RA Nycum L.M., Biegel J.A., Brodeur G.M.,
RT "Cloning and chromosomal localization of the human TRK-B tyrosine
RT kinase receptor gene (NTK2)."
RL Genomics 25:538-546 (1995).
[2]
[2] SEQUENCE FROM N.A. (ISOFORMS TRKB AND TRKB-T1).
RP TISSUE=Brain;
RX MEDLINE=9512473; PubMed=7823156;
RA Shetton D.L., Sutherland J., Gripp J., Camerato T., Armanini M.P.,
RA Phillips H.S., Carroll K., Spencer S.D., Levinson A.D.,
RT "Human trks: molecular cloning, tissue distribution, and expression of
RT extracellular domain immunoadhesins."
RL J. Neurosci. 15:477-491 (1995).
[3]
[3] SEQUENCE FROM N.A. (ISOFORM TRKB-T1).
RP TISSUE=Hippocampus;
RX MEDLINE=95022162; PubMed=7936202; DOI=10.1016/0306-4522(94)90507-X;
RA Allen S.J., Dawbarn D., Eckford S.D., Wilcock G.K., Ashcroft M.,
RA Colebrook S.M., Feeney R., Macgowan S.H.,
RT "Cloning of a non-catalytic form of human trkb and distribution of
RT messenger RNA for trkb in human brain."
RL Neuroscienc 60:825-834 (1994).
[4]
[4] SEQUENCE FROM N.A. (ISOFORMS TRKB; TRKB-T1 AND TRKB-T-SHC).
RP MEDLINE=11656983; PubMed=11798189; DOI=10.1006/dbpc.2001.6301;
RA Stetlow P., Caetren E., Stamm S.,
RT "Analysis of the human trkb gene genomic organization reveals novel
RT trkb isoforms, unusual gene length, and splicing mechanism."
RL Biochem. Biophys. Res. Commun. 290:1054-1065 (2002).
[5]
[5] SEQUENCE FROM N.A. (ISOFORM TRKB-T1), AND VARIANT ARG-309.
RP Steinbeck J.A., Thomsen S., Messig U., Leybold F., Lewerenz J.,
RA Wehner A.,
RT "Full length truncated trkb sequence identified in a screen for genes
RT regulated by ischemic preconditioning.";

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM TRKB-T1).
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477923; DOI=10.1073/pnas.242603899;
 RA Kraussner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik A., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Rabe S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fehley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP DISULFIDE BONDS.
 RX MEDLINE=96004804; PubMed=7574684; DOI=10.1006/abbi.1995.1460;
 RA Hanlu M., Talvenheimo J., Le J., Katta V., Weicher A., Rohde M.F.,
 RT "Extracellular domain of neurotrophin receptor trkB: disulfide
 RT structure, N-glycosylation sites, and ligand binding.";
 RL Arch. Biochem. Biophys. 322:256-264(1995).
 CC -1- FUNCTION: Receptor for brain-derived neurotrophic factor (BDNF),
 CC neurotrophin-3 and neurotrophin-4/5 but not nerve growth factor
 CC (NGF). Involved in the development and/or maintenance of the
 CC nervous system. This is a tyrosine-protein kinase receptor. Known
 CC substrates for the TRK receptors are SHC1, PI-3 kinase, and PLC-
 CC gamma-1.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBUNIT: Exists in a dynamic equilibrium between monomeric (low
 CC affinity) and dimeric (high affinity) structures (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Comment=Additional isoforms seem to exist;
 CC Name=TrkB;
 CC IsoId=O16620-1; Sequence=Displayed;
 CC Name=TrkB-T1;
 CC IsoId=O16620-2; Sequence=VSP_002901, VSP_002902;
 CC Name=TrkB-T-Shc;
 CC IsoId=O16620-3; Sequence=VSP_002903, VSP_002904;
 CC -1- TISSUE SPECIFICITY: Isoform TrkB is widely expressed, mainly in
 CC the nervous tissue. In the CNS, expression is observed in the
 CC cerebral cortex, hippocampus, thalamus, choroid plexus, granular
 CC layer of the cerebellum, brain stem, and spinal cord. In the
 CC peripheral nervous system, it is expressed in many cranial
 CC ganglia, the ophthalmic nerve, the vestibular system, multiple
 CC facial structures, the submaxillary glands, and dorsal root
 CC ganglia. Isoform TrkB-T1 is expressed in multiple tissues, mainly
 CC in brain, pancreas, kidney and heart. Isoform TrkB-T-Shc is
 CC predominantly expressed in brain.
 CC -1- PFM: Ligand-mediated auto-phosphorylation.
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. Insulin
 CC receptor subfamily.
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 2 leucine-rich (LRR) repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U12140; AAC5137.1; -
 CC EMBL: S76473; AAB3109.1; -
 CC EMBL: S76474; AAB3110.1; -
 CC EMBL: X75958; CAA33571.1; -
 CC EMBL: AF410900; AAL67966.1; -
 CC EMBL: AF508964; AAM7876.1; -
 CC EMBL: BC031835; AAH31835.1; -
 CC PIR: A56853; A56853.
 CC PIR: I73631; I73631.
 CC PDB: 1HCF; X-ray; X/Y=283-383.
 CC PDB: 1WMB; X-ray; X=283-385.
 CC Genew; HGNC:8032; NTRK2.
 CC H-invDB; HIX008134; -
 CC MIM: 600456; -
 CC GO: GO:0005887; C: integral to plasma membrane; TAS.
 CC GO: GO:0005015; F: neurotrophin TRKB receptor activity; TAS.
 CC GO: GO:0007169; P: transmembrane receptor protein tyrosine kin. .; TAS.
 CC InterPro: IPR007110; Ig-1Ike.
 CC InterPro: IPR011009; Kinase like.
 CC InterPro: IPR000372; LRR_Nterm.
 CC InterPro: IPR000719; Prot_kinase.
 CC InterPro: IPR002011; ReceptTyKinsII.
 CC InterPro: IPR001245; Tyr_kinase.
 CC InterPro: IPR008266; Tyr_pkinase_AS.
 CC Pfam: PF00447; Ig_1.
 CC Pfam: PF01462; LRRNT; 1.
 CC Pfam: PF00069; Pkinase; 1.
 CC PRINTS: PR00109; TYRKINASE.
 CC PRODOM: PD000001; Prot_kinase; 1.
 CC PROSITE: PS50835; IG_LIKE; 1.
 CC PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 CC PROSITE: PS50011; PROTEIN KINASE DOM; 1.
 CC PROSITE: PS00109; PROTEIN KINASE TYR; 1.
 CC PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
 CC 3D-structure; Alternative splicing; ATP-binding; Glycoprotein;
 CC Immunoglobulin domain; Leucine-rich repeat; Neurogenesis;
 CC Phosphorylation; Polymorphism; Receptor; Repeat; Signal; Transferase;
 CC Transmembrane; Tyrosine-protein kinase.
 CC SIGNAL 1 31
 CC CHAIN 32 822
 CC DOMAIN 32 430
 CC TRANSMEM 431 454
 CC DOMAIN 455 822
 CC REPEAT 72 93
 CC REPEAT 96 117
 CC DOMAIN 197 282
 CC DOMAIN 295 365
 CC NP_BIND 538 807
 CC BINDING 544 552
 CC ACT_SITE 572 572
 CC ACT_SITE 676 676
 CC DISULFID 36 38
 CC DISULFID 32 45
 CC DISULFID 152 176
 CC DISULFID 154 194
 CC DISULFID 218 266
 CC DISULFID 302 345
 CC MOD_RES 516 516
 CC MOD_RES 702 702
 CC MOD_RES 706 706
 CC MOD_RES 707 707
 CC MOD_RES 817 817
 CC MOD_RES 817 817
 CC SITE 516 516
 CC SITE 817 817
 CC FT
 CC Phosphotyrosine (by autocatalysis) (By
 CC similarity).
 CC Phosphotyrosine (by autocatalysis) (By
 CC similarity).
 CC Phosphotyrosine (by autocatalysis) (By
 CC similarity).
 CC Phosphotyrosine (by autocatalysis) (By
 CC similarity).
 CC Phosphotyrosine (by autocatalysis) (By
 CC similarity).
 CC Interaction with SHC1 (By similarity).
 CC Interaction with PLC-gamma-1 (By
 CC similarity).

```

FT CARBOHD 67 67 N-linked (GlcNAc. . .) (Potential) .
FT CARBOHD 95 95 N-linked (GlcNAc. . .) (Potential) .

Query Match 100.0%; Score 4419; DB 1; Length 822;
Best Local Similarity 100.0%; Pred. No. 4,4e-251;
Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSWIRMHGPMARMLMGFCMLVGFWRRAAFACPTSCCKSASRIMCSDPSPGIVAFPRLEP 60
DB 1 MSSWIRMHGPMARMLMGFCMLVGFWRRAAFACPTSCCKSASRIMCSDPSPGIVAFPRLEP 60
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DB 61 NSVDPENITTEIFIANOKRLEIINEDDVEAYVGLRNLTIVDSGLKFAVAKAFKNSNLQHI 120
QY 121 NPTNKLTSLSRKPRHLDISELLIVGNPFTCSQDIMIKTLQKAKSSPDQDLYCLNES 180
DB 121 NPTNKLTSLSRKPRHLDISELLIVGNPFTCSQDIMIKTLQKAKSSPDQDLYCLNES 180
QY 181 SKNIPLANLOIPNCGLPANLAAPNLVTEEGKSITLSCSVAGDPVPMNYMDVGNLVSKHM 240
DB 181 SKNIPLANLOIPNCGLPANLAAPNLVTEEGKSITLSCSVAGDPVPMNYMDVGNLVSKHM 240
QY 241 NETSHTOGSLRITNISDDSGKQISCVAEMLVGEDQDSVNLTVHAPPTITFLASPTSDH 300
DB 241 NETSHTOGSLRITNISDDSGKQISCVAEMLVGEDQDSVNLTVHAPPTITFLASPTSDH 300
QY 301 WCIPFTYKGNKPKALQWRYNAAIINSEKTYCTKHVTNHTHYHGLQDNDPTNHNNGDYT 360
DB 301 WCIPFTYKGNKPKALQWRYNAAIINSEKTYCTKHVTNHTHYHGLQDNDPTNHNNGDYT 360
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DB 361 LIAKNEYGKDEKQISAHFMGWPIDGDPANPNVPIYEDYGTAAANDIGDTTNRSEIPIST 420
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DB 421 DVTDKTGREHLVYAVVIVASVGECLLWMLFLKLAKHSKFGMKGPASVISNDDASAP 480
QY 481 LHHISNGSTSSSSGGPDVAITIGMTKPIVENPQYFISITSLQKPDVFVHKKHNTVL 540
DB 481 LHHISNGSTSSSSGGPDVAITIGMTKPIVENPQYFISITSLQKPDVFVHKKHNTVL 540
QY 541 KREIAGEGAFKGYFLAECYNLCPEODKILVAVKTLDAADNARKDHFRAEHLITNLQHEHI 600
DB 541 KREIAGEGAFKGYFLAECYNLCPEODKILVAVKTLDAADNARKDHFRAEHLITNLQHEHI 600
QY 601 VKFYGVCEGDPILWVFYMGHGDINKFLRAHGPDAVMAAGNPTELTOGOMLHIAQOI 660
DB 601 VKFYGVCEGDPILWVFYMGHGDINKFLRAHGPDAVMAAGNPTELTOGOMLHIAQOI 660
QY 661 AAGMYVYLAHQFVHRDLATRNCLVGENLLVKIGDFGMSRDVYSTDYVGVGHMLPIRWM 720
DB 661 AAGMYVYLAHQFVHRDLATRNCLVGENLLVKIGDFGMSRDVYSTDYVGVGHMLPIRWM 720
QY 721 PPESTMYKFTTESVWLSGLVLMELFTYGKOPWQUSNNVYICITIGQVLTQRPRTPO 780
DB 721 PPESTMYKFTTESVWLSGLVLMELFTYGKOPWQUSNNVYICITIGQVLTQRPRTPO 780
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DB 781 EYVELMLGCMQREPHMKIKIGITLONLAKASPVYDIILG 822

RESULT 2
Q8WKJ7 PRELIMINARY; PRT; 838 AA.
AC Q8WKJ7;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Neutrophin receptor tyrosine kinase type 2.
GN Name=NTRK2;

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Db 361 LIANEGGCKBQJSAHFMGPGIDDANPNPVITEDGTANDIGDTTNSNEIPST 420
 QY 421 DVTDKTGREHLSVYAVVAVVAVVAVGFCLLVLMFLKJLARSKPKMK----- 465
 Db 421 DVTDKTGREHLSVYAVVAVVAVVAVGFCLLVLMFLKJLARSKPKMKDSWFGKVKSRG 480
 QY 466 -GPRSVISNDDSDASPLHHISNGSNTSSSGGPDVAITIGTKIPVIENTPOYFQITNSOL 524
 Db 481 VGPASVISNDDSDASPLHHISNGSNTSSSGGPDVAITIGTKIPVIENTPOYFQITNSOL 540
 QY 525 KPDPFVQIKRHNVLKREIGEGAFKGYFLABECNLCPEODKILVAKTLKXASDNARKD 584
 Db 541 KPDPFVQIKRHNVLKREIGEGAFKGYFLABECNLCPEODKILVAKTLKXASDNARKD 600
 QY 585 FHREABLLTNLOHEHIVKFGVGVCEGDPDLINVEFYMKHGLDKELRAHGPDAVLAEGNP 644
 Db 601 FHREABLLTNLOHEHIVKFGVGVCEGDPDLINVEFYMKHGLDKELRAHGPDAVLAEGNP 660
 QY 645 PTELTGSGMLHIAQOIAAGVYLLASQHFVRDLATNCLVGENILVKIGDFGMSRDVYST 704
 Db 661 PTELTGSGMLHIAQOIAAGVYLLASQHFVRDLATNCLVGENILVKIGDFGMSRDVYST 720
 QY 705 DYRVGSHITMLPIKMPPESTIMRKFTTESDVSLSGVLMIEITYGKOPWYOUSNNEVIE 764
 Db 721 DYRVGSHITMLPIKMPPESTIMRKFTTESDVSLSGVLMIEITYGKOPWYOUSNNEVIE 780
 QY 765 CITGGRVLOBPRTCPQEVYELMLGCMQREPRMRNKIIGITLLONLAKASPVYLDILG 822
 Db 781 CITGGRVLOBPRTCPQEVYELMLGCMQREPRMRNKIIGITLLONLAKASPVYLDILG 838

RESULT 3
 TRKB MOUSE STANDARD; PRT; 821 AA.

ID TRKB MOUSE STANDARD; PRT; 821 AA.
 AC P15209; O91XJ9;
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE BDNF/NT-3 growth factors receptor precursor (BC 2.7.1.112) (TrkB
 DE tyrosine kinase) (GP145-TrkB/GP95-TrkB) (Trk-B).
 GN Name=Trk2; Synonyms=Trkb;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM GP145-TRKB).
 RC TISSUE=Brain;
 RA MEDLINE=90059970; PubMed=2555172;
 RX Klein R., Parada L.F., Coulier F., Barbacid M.;
 RT "trkb, a novel tyrosine protein kinase receptor expressed during mouse
 RT neural development.";
 RL EMBO J. 8:3701-3709(1989).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS GP145-TRKB AND GP95-TRKB).
 RC TISSUE=Brain;
 RX MEDLINE=90263089; PubMed=2160854; DOI=10.1016/0092-8674(90)90476-U;
 RA Klein R., Conway D., Parada L.F., Barbacid M.;
 RT "The trkb tyrosine protein kinase gene codes for a second neurogenic
 RT receptor that lacks the catalytic kinase domain.";
 RL Cell 61:647-656(1990).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM GP95-TRKB).
 RC STRAIN=ND; TISSUE=Thymus;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi U., Bono H., Kondo S.,
 RA Nakai T., Oseko N., Saito R., Suzuki H., Yamana T., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,
 RA Badaricelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schiraldi L.M., Knappin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Brant D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
 RA Datta E., Dregant T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gaasterland T., Gariboldi M., Giesel C., Godzik A., Gough J.,
 RA Grimmond S., Guertlich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.U.,
 RA Konegaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Meglath D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagasima T., Numata K., Okido T., Paven M.J., Pereira G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Tarekna Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Vardaro R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Williams L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Waki K., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Haseizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Ysunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS L1 AND L10).
 RC TISSUE=Trigeminal ganglion;
 RX MEDLINE=97294706; PubMed=9148911; DOI=10.1074/jbc.272.20.13019;
 RA Ninkina N., Grashchuk M., Buchman V.L., Davies A.M.;
 RT "Trkb variants with deletions in the leucine-rich motifs of the
 RT extracellular domain";
 RL J. Biol. Chem. 272:13019-13025(1997).
 RN [5]
 RP FUNCTION.
 RA MEDLINE=91249395; PubMed=1645620; DOI=10.1016/0092-8674(91)90396-G;
 RA Soppet D., Escandon E., Maragos J., Middlemas D.S., Reid S.W.,
 RA Blair J., Burton L.E., Stanton B.R., Kaplan D.R., Hunter T.,
 RA Nicolls K., Parada L.F.;
 RT "The neurotrophic factors brain-derived neurotrophic factor and
 RT neurotrophin-3 are ligands for the trkb tyrosine kinase receptor.";
 RL Cell 65:895-903(1991).
 CC -1- FUNCTION: Receptor for brain-derived neurotrophic factor (BDNF),
 CC neurotrophin-3 and neurotrophin-4/5 but not nerve growth factor
 CC (NGF). Involved in the development and/or maintenance of the
 CC nervous system. This is a tyrosine-protein kinase receptor. Known
 CC substrates for the Trk receptors are Shc1, Pl-3 kinase, and PLC-
 CC gamma-1.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBUNIT: Exists in a dynamic equilibrium between monomeric (low
 CC affinity) and dimeric (high affinity) structures.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Bvent=Alternative splicing; Named isoforms=4;
 CC Comment=Additional isoforms seem to exist;
 CC Name=GP145-TRKB; Synonyms=I3;
 CC IsoId=GP15209-1; Sequence=Displayed;
 CC Name=GP95-TRKB; Synonyms=TI;
 CC IsoId=GP15209-2; Sequence=VSP_002908, VSP_002909;
 CC Name=L1;
 CC IsoId=GP15209-3; Sequence=VSP_002907;
 CC Name=L10;
 CC IsoId=GP15209-4; Sequence=VSP_002905, VSP_002906;
 CC -1- TISSUE SPECIFICITY: The different forms are differentially
 CC expressed in various cell types.
 CC -1- PTM: Ligand-mediated auto-phosphorylation.
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. Insulin
 CC receptor subfamily.
 CC -1- SIMILARITY: Contains 2 leucine-rich (LRR) repeats.
 CC -----
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation in
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way

Query Match	Best Local Similarity	Score	DB 1	Length	821
Matches	772	Conservative	27	Mismatches	22
				Indels	1
				Gaps	1
FT CARBOHYD	67	67	N-linked (GlcNAc. . .)	(Potential)	
FT CARBOHYD	95	95	N-linked (GlcNAc. . .)	(Potential)	
FT CARBOHYD	121	121	N-linked (GlcNAc. . .)	(Potential)	
FT CARBOHYD	178	178	N-linked (GlcNAc. . .)	(Potential)	
FT CARBOHYD	205	205	N-linked (GlcNAc. . .)	(Potential)	
FT CARBOHYD	241	241	N-linked (GlcNAc. . .)	(Potential)	
FT CARBOHYD	254	254	N-linked (GlcNAc. . .)	(Potential)	
FT CARBOHYD	280	280	N-linked (GlcNAc. . .)	(Potential)	
FT CARBOHYD	325	325	N-linked (GlcNAc. . .)	(Potential)	
FT CARBOHYD	338	338	N-linked (GlcNAc. . .)	(Potential)	
FT CARBOHYD	411	411	N-linked (GlcNAc. . .)	(Potential)	
FT VASPPLIC	71	71	I -> M (in isoform L10).		
FT VASPPLIC	72	143	/FtId=VSP_002905.		
FT VASPPLIC	72	143	Missing (in isoform L10).		
FT VASPPLIC	72	143	/FtId=VSP_002906.		
Query Match	94.6%	Score	4179.5	DB 1	Length 821
Best Local Similarity	93.9%	Pred. No.	5e-237		
Matches	772	Conservative	27	Mismatches	22
				Indels	1
				Gaps	1
1	MSWIRHNGPAMARLMGFCWLVYGFMPRAACEPTCKSCASARIWCSDPESGIVAPRLBP	60			
1	MSPPLKMGHGMARLMKLCILVIGFMRASLACTPCKSCSARLWCTEBSGIVAFRLBP	60			
61	NSVDPENITELFIANQRLIEINDEDEAYVGLRNLTIVDSGLKFAAHKAFKNSNLQHT	120			
61	NSVDPENITELFIANQRLIEINDEDEAYVGLRNLTIVDSGLKFAAHKAFKNSNLQHT	120			
121	NFTNKLTSLSRGRFRLLDSELLVGNPPTGSCDLMWITTLIOBAKSSPTOTOLYCLNES	180			
121	NFTNKLTSLSRGRFRLLDSELLVGNPPTGSCDLMWITTLIOBAKSSPTOTOLYCLNES	180			
181	SKNIPPLANTLOIPNGCLPSAMLAAPNLVTEBGSITLSCSAVDGPVPMVMDVGNLVSCKM	240			
181	SKNIPPLANTLOIPNGCLPSARLAPNLVTEBGSKVTLSCSVGSDPLPRLYVDGNLVSCKM	240			
241	NETSHTGQSLRITNISDSDSGKOISCVAEMLVGBDDSVNLTVHFAPTITFLESPTSDDH	300			
241	NETSHTGQSLRITNISDSDSGKOISCVAEMLVGBDDSVNLTVHFAPTITFLESPTSDDH	300			
301	WCIPFYTKGNPKPALQWFFNGALLNESKTYCTKIHTNTHETHYGCLQDLPPTHMNGDYT	360			
301	WCIPFYTKGNPKPALQWFFNGALLNESKTYCTKIHTNTHETHYGCLQDLPPTHMNGDYT	360			
361	LIAKNEYGKGEKOISAHFMGMPGIDOCANPNYPDVITYEDVGTAAINDIGDTTNSNEIPST	420			
361	LMAKNEYGKGEKOISAHFMGMPGIDVETNPNYBEVLIED-TPPTDGGDTTNSNEIPST	419			
421	DVTDKTRGRELHVSVAVVIVASVGFCLLVMLPFLKTLARSHKFGMKGPASVYSNDDDSASP	480			
421	DVTDKTRGRELHVSVAVVIVASVGFCLLVMLPFLKTLARSHKFGMKGPASVYSNDDDSASP	480			
481	LHHISNGSNTPSSSEGGPDVITIGMTKIPIYENPOYFGITNSOLKPDTPYQHKRHNIVL	540			
481	LHHISNGSNTPSSSEGGPDVITIGMTKIPIYENPOYFGITNSOLKPDTPYQHKRHNIVL	540			
541	KREIGEGAFGVFLAECVNLCPRODKTLVAVKTLKQASDARADFPREAVLTNLQHEHI	600			
541	KREIGEGAFGVFLAECVNLCPRODKTLVAVKTLKQASDARADFPREAVLTNLQHEHI	600			
601	VKPYGVCEVGPDLIMVEYMKGGDLNFKLFAHGPDAVLAAEGNPPELTQSQMLHAQOI	660			
601	VKPYGVCEVGPDLIMVEYMKGGDLNFKLFAHGPDAVLAAEGNPPELTQSQMLHAQOI	660			
661	AAGNVYTLASQHFVHRDLATNCLVGENLVKIGDPFGMSRDVYSTDYRNGGHTMLPIRMW	720			
661	AAGNVYTLASQHFVHRDLATNCLVGENLVKIGDPFGMSRDVYSTDYRNGGHTMLPIRMW	720			
721	PPSIRIMRKFTTSDVSLGVLMELFTYKQKQMYOLSNNEVECTTQGVLORPPTCPQ	780			
721	PPSIRIMRKFTTSDVSLGVLMELFTYKQKQMYOLSNNEVECTTQGVLORPPTCPQ	780			
781	EVEELMAGCQWRBEPHMKNIKGIHTLLQNLAKSPVYLDILG	822			

FT VARSPLIC 477 821 /FtId=VSP_002910. Missing (in isoform T1).
 FT VARSPLIC 466 474 /FtId=VSP_002911. PASVISND -> KOKAYFAS (in isoform T2).
 FT VARSPLIC 475 821 /FtId=VSP_002912. Missing (in isoform T2).
 SQ SEQUENCE 821 AA; 92186 MW; 0DDACDA12CDAA0E CRC64;
 Query Match 94.2%; Score 4162.5; DB 1; Length 821;
 Best Local Similarity 93.6%; Pred. No. 5e-236;
 Matches 769; Conservative 25; Mismatches 27; Indels 1; Gaps 1;

QY 1 MSSWIRHNGPAMARLWGFVGVFRAFAFACPTSCCKSASRIWCSDPSPGIVAFPRLEP 60
 1 MSPFPRHNGPAMARLWGFVGVFRAFAFACPTSCCKSASRIWCSDPSPGIVAFPRLEP 60
 DB 1 NFRANKLTSISRKHFRHLDSELLVGNPFTSCDIMWIKTLQBAKSPPTQDLYCLNES 180
 121 NFRANKLTSISRKHFRHLDSELLVGNPFTSCDIMWIKTLQBAKSPPTQDLYCLNES 180
 121 NFRANKLTSISRKHFRHLDSELLVGNPFTSCDIMWIKTLQBAKSPPTQDLYCLNES 180
 QY 181 SKNPLPLANTQIPNGLSPARLAAPNLVYBESKSTISCSVAGDVPVPMYVGNLVSKM 240
 181 SKNPLPLANTQIPNGLSPARLAAPNLVYBESKSTISCSVAGDVPVPMYVGNLVSKM 240
 DB 181 SKNPLPLANTQIPNGLSPARLAAPNLVYBESKSTISCSVAGDVPVPMYVGNLVSKM 240
 241 NETSHGOSLRITINISDDSGKQISCAVENVGEDQSVNLTVHAPATITLESPTSDDH 300
 241 NETSHGOSLRITINISDDSGKQISCAVENVGEDQSVNLTVHAPATITLESPTSDDH 300
 QY 301 WCPBPTKGNPKPALQWPNYNGALINESKYICTKHVNHTEHOCLODNPTHANNQDYT 360
 301 WCPBPTKGNPKPALQWPNYNGALINESKYICTKHVNHTEHOCLODNPTHANNQDYT 360
 DB 301 WCPBPTKGNPKPALQWPNYNGALINESKYICTKHVNHTEHOCLODNPTHANNQDYT 360
 361 LIANEVGEKDEKQISAFPMGPIGDDGAPNYPVPIYEDVGTANDIGDTNRSENEIPST 420
 361 LIANEVGEKDEKQISAFPMGPIGDDGAPNYPVPIYEDVGTANDIGDTNRSENEIPST 420
 DB 361 LIANEVGEKDEKQISAFPMGPIGDDGAPNYPVPIYEDVGTANDIGDTNRSENEIPST 420
 421 DVADQTRREHLVYAVVAVVAVSVFCLLMFLMLKLARSHKFKGKSPASVISNDD9ASP 480
 421 DVADQTRREHLVYAVVAVVAVSVFCLLMFLMLKLARSHKFKGKSPASVISNDD9ASP 480
 DB 421 DVADQTRREHLVYAVVAVVAVSVFCLLMFLMLKLARSHKFKGKSPASVISNDD9ASP 480
 481 LHHISNSNSNPSSSEGGPDVATIGMTKIPVLENPOYGTITNSOLKPDTPVGHIRAHIVL 540
 481 LHHISNSNSNPSSSEGGPDVATIGMTKIPVLENPOYGTITNSOLKPDTPVGHIRAHIVL 540
 DB 481 LHHISNSNSNPSSSEGGPDVATIGMTKIPVLENPOYGTITNSOLKPDTPVGHIRAHIVL 540
 541 KRELGEAGFGKVFIAECYNLCPEODKILVAVKTLKXASDNARKDFFHREABLLTNLOHEHI 600
 541 KRELGEAGFGKVFIAECYNLCPEODKILVAVKTLKXASDNARKDFFHREABLLTNLOHEHI 600
 DB 541 KRELGEAGFGKVFIAECYNLCPEODKILVAVKTLKXASDNARKDFFHREABLLTNLOHEHI 600
 601 VKFYGVCVEGDPPLIMVEYMGKGLNKLFLRAHGPDAVLMAGNPTELTOGOMLHIAQOI 660
 601 VKFYGVCVEGDPPLIMVEYMGKGLNKLFLRAHGPDAVLMAGNPTELTOGOMLHIAQOI 660
 DB 601 VKFYGVCVEGDPPLIMVEYMGKGLNKLFLRAHGPDAVLMAGNPTELTOGOMLHIAQOI 660
 661 AAGGVYIASQHFVARDLATRNCLVGENLVKIGPFGMSRDVYSTDYRVGCHTMLPIRMM 720
 661 AAGGVYIASQHFVARDLATRNCLVGENLVKIGPFGMSRDVYSTDYRVGCHTMLPIRMM 720
 DB 661 AAGGVYIASQHFVARDLATRNCLVGENLVKIGPFGMSRDVYSTDYRVGCHTMLPIRMM 720
 721 PPSISIMRKFTTESDWSISGVLMWEIFYTGKOPYQUSNNVEICTIOGRULORPRICPO 780
 721 PPSISIMRKFTTESDWSISGVLMWEIFYTGKOPYQUSNNVEICTIOGRULORPRICPO 780
 DB 721 PPSISIMRKFTTESDWSISGVLMWEIFYTGKOPYQUSNNVEICTIOGRULORPRICPO 780
 781 EVELMLGCMQREBPMRNKINGITLLQNLAKASPVYLDILG 822
 781 EVELMLGCMQREBPMRNKINGITLLQNLAKASPVYLDILG 822
 DB 781 EVELMLGCMQREBPMRNKINGITLLQNLAKASPVYLDILG 822

AC Q91987; Q91010;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE BDNF/NT-3 growth factors receptor precursor (EC 2.7.1.112) (TrkB
 DE tyrosine kinase) (Trk-B).
 OS Name=TrkB;
 GN Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 10).
 RC TISSUE=Brain;
 RX MEDLINE=95047511; PubMed=7959025; DOI=10.1016/0378-1119(94)90184-8;
 RA Vilh N., Erdmann K., Heumann R.;
 RT "Cloning and sequence analysis of a cDNA encoding a novel truncated
 RT form of the chicken TrkB receptor.";
 RL Gene 149:383-384 (1994).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=94116452; PubMed=8287802;
 RA Dechant G., Biffo S., Okazawa H., Kolbeck R., Pottgiesser J.,
 RA Barde Y.-A.;
 RT "Expression and binding characteristics of the BDNF receptor chick
 RT trkB.";
 RL Development 119:545-558 (1993).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE FROM N.A.
 RP (ISOFORMS 2; 3; 4; 5; 6; 7; 8; 9; 10; 11 AND 12).
 RX MEDLINE=96370546; PubMed=8774442;
 RA Garner A.S., Menegay H.J., Boeshore K.L., Xie X.Y., Vocil J.M.,
 RA Johnson J.E., Large T.H.;
 RT "Expression of TrkB receptor isoforms in the developing avian visual
 RT system.";
 RL J. Neurosci. 16:1740-1752 (1996).
 CC -1- FUNCTION: Receptor for brain-derived neurotrophic factor (BDNF),
 CC neurotrophin-3 and neurotrophin-4/5 but not nerve growth factor
 CC (NGF). Involved in the development and/or maintenance of the
 CC nervous system. This is a tyrosine-protein kinase receptor. Known
 CC substrates for the Trk receptors are Shc1, F1-3 kinase, and PLC-
 CC gamma-1 (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBUNIT: Exists in a dynamic equilibrium between monomeric (low
 CC affinity) and dimeric (high affinity) structures (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Bvent=Alternative splicing; Named isoforms=12;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1; Synonyms=Alpha-Fl;
 CC IsoId=Q91987-1; Sequence=Displayed;
 CC Name=2; Synonyms=Beta-Fl;
 CC IsoId=Q91987-2; Sequence=VSP_002914;
 CC Note=It is uncertain whether Leu-144 or Met-188 is the initiator
 CC of isoform 2;
 CC Name=3; Synonyms=ED;
 CC IsoId=Q91987-3; Sequence=VSP_002915;
 CC Name=4; Synonyms=JD;
 CC IsoId=Q91987-4; Sequence=VSP_002923;
 CC Name=5; Synonyms=U1;
 CC IsoId=Q91987-5; Sequence=VSP_002920;
 CC Name=6; Synonyms=Alpha-TL;
 CC IsoId=Q91987-6; Sequence=VSP_002918;
 CC Name=7; Synonyms=U1+TL;
 CC IsoId=Q91987-7; Sequence=VSP_002919;
 CC Name=8; Synonyms=U2+TL;
 CC IsoId=Q91987-8; Sequence=VSP_002918;
 CC Name=9; Synonyms=ED U2+TL;
 CC IsoId=Q91987-9; Sequence=VSP_002915;
 CC Name=10; Synonyms=U1+U2+TL;
 CC VSP_002921;

[illegible]

FT	MOD_RES	813	813		similarity).
FT	SITE	512	512		Phosphotyrosine (by autocatalysis) (By similarity).
FT	SITE	613	813		Interaction with SHC1 (By similarity). Interaction with PLC-gamma-1 (By similarity).
FT	CARBOHYD	66	66		N-linked (GlcNAc . .) (potential).
FT	CARBOHYD	94	94		N-linked (GlcNAc . .) (potential).
FT	CARBOHYD	120	120		N-linked (GlcNAc . .) (potential).
FT	CARBOHYD	199	199		N-linked (GlcNAc . .) (potential).
FT	CARBOHYD	204	204		N-linked (GlcNAc . .) (potential).
FT	CARBOHYD	226	226		N-linked (GlcNAc . .) (potential).
FT	CARBOHYD	253	253		N-linked (GlcNAc . .) (potential).
FT	CARBOHYD	287	287		N-linked (GlcNAc . .) (potential).
FT	CARBOHYD	324	324		N-linked (GlcNAc . .) (potential).
FT	CARBOHYD	337	337		N-linked (GlcNAc . .) (potential).
FT	CARBOHYD	408	408		N-linked (GlcNAc . .) (potential).
FT	VARSPLIC	1	187		Missing (in isoform 2).
FT	VARSPLIC				/FtId=VSP_002914.
FT	VARSPLIC	384	394		Missing (in isoform 3, isoform 9 and isoform 12).
FT	VARSPLIC				/FtId=VSP_002915.
FT	VARSPLIC	462	467		GPSYI -> RGRRK (in isoform 11).
FT	VARSPLIC	468	818		Missing (in isoform 11).
FT	VARSPLIC	463	473		/FtId=VSP_002917.
FT	VARSPLIC				PSSVSINDDS -> FVLPHKIPIDG (in isoform 6, isoform 7, isoform 8, isoform 9, isoform 10 and isoform 12).
FT	VARSPLIC	474	818		/FtId=VSP_002918.
FT	VARSPLIC				Missing (in isoform 6, isoform 7, isoform 8, isoform 9, isoform 10 and isoform 12).
FT	VARSPLIC	462	462		G -> VHGSEVGKGLVDQIMWLSLQDCNDEG (in isoform 5 and isoform 7).
FT	VARSPLIC				/FtId=VSP_002920.
FT	VARSPLIC	462	462		G -> EQMVTAVNSDVHNHNSRASNRLG (in isoform 8 and isoform 9).
FT	VARSPLIC	462	462		/FtId=VSP_002921.
FT	VARSPLIC	462	462		G -> VHGEVGKGLVDQIMWLSLQDCNDEGMVTVNSDVH NSNSTASDNRLG (in isoform 10 and isoform 12).
FT	VARSPLIC	462	465		/FtId=VSP_002922.
FT	VARSPLIC	462	465		Missing (in isoform 4).
FT	VARSPLIC				/FtId=VSP_002923.
FT	SEQUENCE	818 AA;	91736 MW;		D1BA39E2092B2152 CRC64;
Query Match:		77.5%;	Score 3426;	DB 1;	Length 818;
Beet Local Similarity		77.6%;	Pred. No. 8.7e-193;		
Matches 638;		Conservative	73;	Mismatches 107;	Indels 4; Gaps 3
QY	1	MSWIRMGPMARLMGFOWVMRAAFACPTSCSKSASRIICSDPEPGIVAPRLRP	60		
Db	1	MYSWRRRRGPGIARLMGLCCVLVCGKRQALGCPASCRCSSMRINCSBPVIGITSTP-VQ	59		
QY	61	NSVDPENITEIFIANOKLEIINEEDVEAYVGLRMILIVSGLKFAVAKFLKSNLOHI	120		
Db	60	RSTEDDNTETIYIANQRKLDESINDNEVPYVGLKNLTIVDSGLRFVSRQAFCYNINLYI	119		
QY	121	NFTNRKLTSLSRKHRRHLDSLIIIVGNPFYCSCDIMIKTLIQEAKSSPDITODLYCLANS	180		
Db	120	NLSRNKLSSLKKPRRHGLSDLIIIVDNPKFSCSIIMWKQETKFYEADIDYCVDN	179		
QY	181	SKNIPLANLOTNCLPSANTLAAPLVTEBGSKITLSCSVADPVPNMWADVGNVSKM	240		
Db	180	NKRILAMDKKPCNDLPBANLSTNNVIITYEGSITLLCDITTGPPPNVSMVLNLVSRHE	239		
QY	241	NETSHTOGSLRTINISDDSGKOISCVAEMLVGEDODSVNLTVHAPITTFLESPTSDH	300		
Db	240	SOTSNGRPSLTIKVNVSSMDSGLMISCVAENIVGEVOTSAELTVFPAPNITTFIESPTPDH	299		
QY	301	WCIPPTVGNPKPALQWRYNGAILEBSKITCYKIHYTNHTETHGCLQDLNPTHANNGDYT	360		

Db 300 WCIFPTKGNKPKPLQWFBGAIINBSRYICTKHVINOSEHYGCLQDNPHTLHNGAVT 359
 Qy 361 LIANEXGKDEKQISAHFMWPGIDGANNPYPVVIEDYGTAAIDGTTNRSNEIPST 420
 Db 360 LIANEXGEDEKRDADAHMSVPG--DSSGFLVDDPYVE-YETTTNDLGDTTNSNQITSP 416
 Qy 421 DVTDKTGRHLSVYAVVAVIASVVGFCILVMLFLKLARHSFKMGKSPASVISNDDASAP 480
 Db 417 DVSNKNEKEDSITVYVVVGVIAALVCTGLVIMLIILKFGHRSFKMGKSPASVISNDDASAP 476
 Qy 481 LHHISNSNTSPSSSEGGPDVAVIIGMTKIPVLENPOYRITTSOLKPDPTFVGHIRKHNIVL 540
 Db 477 LHHISNSNTSPSSSEGGPDVAVIIGMTKIPVLENPOYRITTSOLKPDPTFVGHIRKHNIVL 536
 Qy 541 KRELGEAGFGKVFALAEACYNLCPEODKILAVKTLKDASDNARKPFHRAELTLNLOHEHI 600
 Db 537 KRELGEAGFGKVFALAEACYNLCPEODKILAVKTLKDASDNARKPFHRAELTLNLOHEHI 596
 Qy 601 VKFYGVCEVGDPLIMVEFYMKHGDINKFLRAHGPDAVLMAEGNPTELITQSOMLHIAQOI 660
 Db 597 VKFYGVCEVGDPLIMVEFYMKHGDINKFLRAHGPDAVLMAEGNPTELITQSOMLHIAQOI 656
 Qy 661 AAGNMYLASQHFVRDLATRNCLVGENLVKIGDPMGRSDVYSTDYRVGHTMLPIRM 720
 Db 657 AAGNMYLASQHFVRDLATRNCLVGENLVKIGDPMGRSDVYSTDYRVGHTMLPIRM 716
 Qy 721 PPSIMTRKFTTESDVMISGLVVLWEIFTYGGKOPWYOLSNNVEICTQGRVLOPRTCPO 780
 Db 717 PPSIMTRKFTTESDVMISGLVVLWEIFTYGGKOPWYOLSNNVEICTQGRVLOPRTCPO 776
 Qy 781 EVELMLGCMQREBPMRNKIKGIHTLLQNLAKASPVYLDIIG 822
 Db 777 EYVDLMGCMQREBPMRNKIKGIHTLLQNLAKASPVYLDIIG 818

RESULT 6

Q9YH44 PRELIMINARY; PRT; 821 AA.

AC Q9YH44
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Neurotrophin receptor B xtrkb-alpha.
 GN Name=xtrkb;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 NC NCB1_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97101727; PubMed=8946245;
 RA Islam N., Gagnon F., Moss T.;
 RT "Catalytic and non-catalytic forms of the neurotrophin receptor xtrkb
 RT mRNA are expressed in a pseudo-segmental manner within the early
 RT Xenopus central nervous system."
 RL Int. J. Dev. Biol. 40:973-983(1996).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin
 CC receptor subfamily.
 DR EMBL: U39670; AAD00001.1; -.
 DR HSBP; 016620; IWB.
 DR GO: GO:00016021; C: integral to membrane; IEA.
 DR GO: GO:0005524; F: ATP binding; IEA.
 DR GO: GO:0004872; F: receptor activity; IEA.
 DR GO: GO:0016740; F: transferase activity; IEA.
 DR GO: GO:0004714; F: transmembrane receptor protein tyrosine kin. . .; IEA.
 DR GO: GO:0006468; P: protein amino acid phosphorylation; IEA.
 DR GO: GO:0007169; P: transmembrane receptor protein tyrosine kin. . .; IEA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR011009; Kinase_like.

DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002011; Receptcytkinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008265; Tyr_kinase_AS.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00082; LRCT; 1.
 DR SMART; SM00219; TYRCK; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
 KW ATP-binding; Kinase; Phosphorylation; Receptor; Transferase;
 KW Transmembrane; Tyrosine-protein kinase.
 SQ SEQUENCE 821 AA; 92311 MW; 0AF81BE74FDBFED3 CRC64;

Query Match 70.0%; Score 3091.5; DB 2; Length 821;
 Best Local Similarity 71.5%; Pred. No. 3.8e-1173;
 Matches 591; Conservative 88; Mismatches 137; Indels 11; Gaps 9;

Qy 1 MSSWIRHGGPAMARLMGFCWLIVG-FWRAFACTSCCKCSASRIWCSDFGIVAPRLE 59
 Db 1 MRLWKSGHGPDLVEVYGALMILALFWR-GLACPQYCSNSTRITWCTLMKGIAAFVYLE 59
 Qy 60 PNVSDPENITEIFLANKRLIINEDDVEAVGVRLITVDSGLKFAVAKAPLKSNSLOH 119
 Db 60 DSSL-AENITDVIYANORSLASINDDVKIYTGRLNLTVDVGQIVSRQAFRNKLKLT 118
 Qy 120 INFRNKLTLSLRGPHRLDSEILVGNPPTSCSDIMWIKTLQBAKS-SPDTODLYCLN 178
 Db 119 INFSRNKLTLSITKIFPHLTLISQLLGNPQCSDLMWVYVLETSINMENONHCFN 178
 Qy 179 ESSKNIPLANLIQIPNCGIPSNALAPNLVYBEGSITLSCSVAGDPVPMYMGVNLVSK 238
 Db 179 DNKKKIPLENNHINPCGLPIANVSTVNITVLEGNETTLYCDANGLPDPMWMDISQITSK 238
 Qy 239 HMTSHTQSLRATTNISSDSGKOISCVANLVGEODSVNLVHPAPTTLPESPRSD 298
 Db 239 KRMMAKRPVLLTLKNVTSLDNKKRIIVCAENSGBEHSIVELNVHPVPTTFIDLPILD 298
 Qy 299 HHWCIPPTVGNPAPALOMFPGNAGIINESKYICIKIYHYN--TEYHGCLODNPTRHNN 356
 Db 299 HHWCIPSPVRNPPPTLOMFHGNILSBTDFIWSKHETSNTYTBHHCLOLDSPTLNN 358
 Qy 357 GDVTLAKNEXGDEKQISAHFMWPGIDGANNPYPVVIEDYGTAAIDGTTNRSN 415
 Db 359 GFYTLRAENIYGRBERISALFMKGP--DGS-NP-ITDPGFYDETTSNDIGSTDTIGT 414
 Qy 416 EIPSTDVDTKGRHLSVYAVVAVIASVVGFCILVMLFLKLARHSFKMGKSPASVISND 475
 Db 415 GVTSTDVNSNGENBSITVYVVGVIAALVCTGLVIMLIILKFGHRSFKMGKSPASVISND 474
 Qy 476 DSAEPLHHSNGSTPPSSBGGPDVAVIIGMTKIPVLENPOYRITTSOLKPDPTFVGHIRK 535
 Db 475 DSAEPLHHSNGSTPPSSBGGPDVAVIIGMTKIPVLENPOYRITTSOLKPDPTFVGHIRK 534
 Qy 536 HNIYKRELGEAGKVFALAEACYNLCPEODKILAVVTKLKDASDNARKPFHRAELTLNL 595
 Db 535 HNIYKRELGEAGKVFALAEACYNLYPEODKILAVVTKLKDASDNARKPFHRAELTLNL 594
 Qy 596 QHEHIYFYGVCVGDPLIMVEFYMKHGDINKFLRAHGPDAVLMAEGNPTELITQSOMLH 655
 Db 595 QHEHIYFYGVCVGDPLIMVEFYMKHGDINKFLRAHGPDAVLMAEGNPTELITQSOMLH 654
 Qy 656 IAAQIAGMYLASQHFVRDLATRNCLVGENLVKIGDPMGRSDVYSTDYRVGHTML 715
 Db 655 IAAQIAGMYLASQHFVRDLATRNCLVGENLVKIGDPMGRSDVYSTDYRVGHTML 714
 Qy 716 PIRMPPEIMTRKFTTESDVMISGLVVLWEIFTYGGKOPWYOLSNNVEICTQGRVLOPR 775

Db 715 PIRMPPEESIMYKRTTESDVMSLGVLMELFTYGKOPWYQLSNNEVIECTIGRVLQRP 774
 QY 776 RTCPQVEYELMLGCMQREPHMRKNIKGIHTLLONLAKASPVYLDIIG 822
 Db 775 RTCPKEVYDMLGCMQREPHMRKNIKGIHTLLONLAKASPVYLDIIG 821

RESULT 7
 QYH43 PRELIMINARY; PRT; 811 AA.
 ID QYH43
 AC QYH43;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
 DE Neurotrophin receptor B xtkB-alpha.
 GN Name=xtkB;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
 OC Xenopodidae; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97101727; PubMed=8946245;
 RA Islam N., Gagnon F., Moss T.;
 RT "Catalytic and non-catalytic forms of the neurotrophin receptor xtkB
 mRNA are expressed in a pseudo-segmental manner within the early
 RT Xenopus central nervous system.";
 RL Int. J. Dev. Biol. 40:973-983(1996).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin
 CC receptor subfamily.
 CC EMBL; U39671; AAD00002.1; -.
 DR HSSP; Q16620; 1MBB.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR011009; Kinase_1like.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR000719; Prot. kinase.
 DR InterPro; IPR002011; ReceptLyrKinsII.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00409; IG_1_kinase; 1.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS00239; RECEPTOR TYR_KIN_II; 1.
 KW ATP-binding; Kinase; Phosphorylation; Receptor; Transferase;
 KW Transmembrane; Tyrosine-protein kinase.
 SQ SSOURCE 811 AA; 91249 MW; CE7CDICF132C1CFS CRC64;

Query Match 69.7%; Score 3078.5; DB 2; Length 811;
 Best Local Similarity 71.0%; Pred. No. 2.2e-172;
 Matches 587; Conservative 87; Mismatches 132; Indels 21; Gaps 8;

QY 1 MSSVIRHMGAMARLWGFCLVVG-FVRAAFACPTSCSCASRIKSDPSFGIYAFPRLE 59
 Db 1 MRLMKSGHGDPLVEYGLMTLLAFWR-GLACQYSCSCTRIMCTLMKGIAPFVLE 59
 QY 60 PMSVDPENITEIFIANOKRLIINEDDVEAYVGLRLITVDSGLKFAHKAFLKNSNLQH 119

Db 60 DSSL-ASNTIDITYANORSLASINDDVKITYGLKRLITVDSGLQIVSRAFRKRLKLT 118
 QY 120 INTRNKLTSLSKRFRHLDISELIVGNPFTSCDIMIKTLQOKAS-SPTODLYCLN 178
 Db 119 INFSRNKLTSLTKKIFRHLTSLQLLGQNFQSCDLMVKVLETJSLMBENONHICFN 178
 QY 179 BSSKNIPLANLQIPNGCLPESANLAAPRLTYEKGSLTLAGCVAGDPVPMYDVNLVSK 238
 Db 179 DNKKIPLFNMHLPNGCLPIANVSTVITLBNBETLLYCDAGLPDPNWSMIDISQI 238
 QY 239 HNMETSHTQSLRTITNISSDPSGKOISCVANLVGSDPSVNTLVHAPITTFLESPTSD 298
 Db 239 KRMEMAKRPVLLTKAVTSLDNKRILYCAENSVGSDHISVELANVHPPITITDLP 298
 QY 299 HNMCIPTVGNPKPALQWFPYNGALINESKYICTKIHVTNH--TEYHGLQDNPTMMN 356
 Db 299 HNMCIPTVGNPKPALQWFPYNGALINESKYICTKIHVTNH--TEYHGLQDNPTMMN 356
 QY 357 GDTTLAKNEYGDEKOISAFPMGPEIDGAPNRPDVLYEDYGRANDIGDT-TKRSN 415
 Db 359 GFTYLAENITVGRDERSISALFMKGP--DD-----DYETTSNDIGGISTDICT 404
 QY 416 EISTDVTDTKGRHLSVYAVVYASVYGFCLVWLFLKLARHSKRGKMPASVTSND 475
 Db 405 GVTSTDSNGNEDSITVYVVGIALVCTGLVIMLILFRGRHSKFGKLGPSVTSND 464
 QY 476 DSASPLHISNGSNTSSSESGPDVAVIGMTKIPVLENPQYFGITNSQLKPDFTVQHKR 535
 Db 465 DSASPLHISNGSNTSSSESGPDVYIGMTKIPVLENPQYFGITNSQLKPDFTVQHKR 524
 QY 536 HNIYKRELGEAGFGKVFLEACYNLCPEODKILVAVKTLKQASDNARKDPRHREALLTNL 595
 Db 525 HNIYKRELGEAGFGKVFLEACYNLCPEODKILVAVKTLKQASDNARKDPRHREALLTNL 584
 QY 596 QHEHIYKFGVGVCEGDPILVFEYMKRGDKNFKLRAHGPVAVMARGNPTELTOGOMLH 655
 Db 585 QHEHIYKFGVGVCEGDPILVFEYMKRGDKNFKLRAHGPVAVMARGNPTELTOGOMLH 644
 QY 656 IAOQIAGWYVLLSOHFVHDLATRNCLVGENLVKIGDFGMSRDVYSTYRVGHTTML 715
 Db 645 IAOQIAGWYVLLSOHFVHDLATRNCLVGENLVKIGDFGMSRDVYSTYRVGHTTML 704
 QY 716 PIRMPPEESIMYKRTTESDVMSLGVLMELFTYGKOPWYQLSNNEVIECTIGRVLQRP 775
 Db 705 PIRMPPEESIMYKRTTESDVMSLGVLMELFTYGKOPWYQLSNNEVIECTIGRVLQRP 764
 QY 776 RTCPQVEYELMLGCMQREPHMRKNIKGIHTLLONLAKASPVYLDIIG 822
 Db 765 RTCPKEVYDMLGCMQREPHMRKNIKGIHTLLONLAKASPVYLDIIG 811

RESULT 8
 QYH43 PRELIMINARY; PRT; 669 AA.
 ID QYH43
 AC QYH43;
 DT 25-OCT-2004 (TREMblrel. 28, Created)
 DT 25-OCT-2004 (TREMblrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)
 DE Tyrosine kinase receptor (Fragment).
 OS Peophila guttata (Zebra finch) (Taeniopygia guttata).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Passeriformes; Estrilidae;
 OC Estrilidae; Taeniopygia.
 NCBI_TaxID=59729;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Agate R.J., Chen X., Itoh Y., Arnold A.P.;
 RT "Cloning and expression of trkB in zebra finch brain.";
 RN Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA Thompson J.F.;

RL Submitted (UTL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin
CC receptor subfamily.
DR EMBL: AY679520; AAT80893.1; -.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0004714; F:transmembrane receptor protein tyrosine kin. .; IEA.
DR GO: GO:0006448; P:protein amino acid phosphorylation; IEA.
DR GO: GO:007169; P:transmembrane receptor protein tyrosine kin. .; IEA.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003599; IG.
DR InterPro: IPR011009; IG c2.
DR InterPro: IPR007119; Prot_kinase.
DR InterPro: IPR007119; Prot_kinase.
DR InterPro: IPR02011; ReceptLTKinase.
DR InterPro: IPR02290; Ser_chr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR InterPro: IPR008266; Tyr_kinase_AS.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF00069; Kinase; 1.
DR Pfam: PF00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00409; IG; 1.
DR SMART: SM00408; IGc2; 1.
DR SMART: SM00220; S_TKC; 1.
DR SMART: SM00219; TYKC; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00109; PROTEIN KINASE_TYR; 1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_1; 1.
DR ATP-binding; Kinase; Phosphorylation; Receptor; Transferase;
KW Transmembrane.
FT NON TER 1 1
SQ SEQUENCE 669 AA; 74749 MW; 8CA583205F76E269 CRC64;
Query Match 65.5%; Score 2896.5; DB 2; Length 669;
Best Local Similarity 80.5%; Pred. No. 8.3e-162;
Matches 540; Conservative 48; Mismatches 80; Indels 3; Gaps 2;
QY 152 CSCDIIMIKTLOEAKSSPDODLYCLINSSKNIPLANQIPNCGLPANLAPMLTVEG 211
DB 2 CSCDIIMIKTLOEAKSSPDODLYCLINSSKNIPLANQIPNCGLPANLAPMLTVEG 61
QY 212 KSITLSCSVAGDPVPMYMDVGNLVSKIMETSHTOGSLRTINISDSDGKQISCAENL 271
DB 62 KSITLYCDTGGPPPNVSWVTNLVSNHESPTNKNPASLTIKNVSMDSGIEISCAENI 121
QY 272 VGEQDSVNLTVHAPITITPLESPTSDHHCIPPTVKGNPKPALQWFTYNGAILNESKYIC 331
DB 122 VGEQDASAEALVFAPAPNITFIESPTPDHMCIPFTVKGNPKPALQWFTYNGAILNESBYIC 181
QY 332 TKIHVHTHTEYHGLQIDNPTHMANGDYTLAKNVEYGEDEKQISAHFPMGAGIDGANGPN 391
DB 182 TKIHVINOSEYHGLQIDNPTHLNGATTLAKNDYGEDEKRVDDHFMFSVGC--DGNQPI 239
QY 392 YPDVIEDYGTANDIGDTTKRSNEIPSTDYTDKTRGHELSVAVVAVVAVGFCLLVML 451
DB 240 LDPDYVE-YETTPNDLDGATNNSNOITSDVSNKENESITVYVVVGIAALVCGIIVTL 298
QY 452 FLTLAHSKFGKMGKPAVSISNDSDASPLHHISNGSTPSSSGGPDVAITIGMTKIPVI 511
DB 299 IILFGHSHKFGKMGKPAVSISNDSDASPLHHISNGSTPSSSGGPDVAITIGMTKIPVI 358
QY 512 ENPQYFGITNSQLPDTFVVOHVKRHNIYVKRELGBGAGKVFALACVNLCEGQKLIYAV 571
DB 359 ENPQYFGITNSQLPDTFVVOHVKRHNIYVKRELGBGAGKVFALACVNLCEGQKLIYAV 418
QY 572 KTLKADASDNARKDPRHRAELLTNLQHEHIVFVYGVCEGDPILVWFETMKGDINKFLRA 631

DB 419 KTLKADASDNARKDPRHRAELLTNLQHEHIVFVYGVCEGDPILVWFETMKGDINKFLRA 478
QY 632 HGPDAVMAESNPTELTOSOMLHIAOOIAAGWYILASQHVHDLATRNCLVGENILYK 691
DB 479 HGPDAVMAESNPTELTOSOMLHIAOOIAAGWYILASQHVHDLATRNCLVGENILYK 538
QY 692 IGDPMGRDVSSTDYVVGHTMLPIRMMPESIMYRKFTTESDVSLSGLVLMETFTYK 751
DB 539 IGDPMGRDVSSTDYVVGHTMLPIRMMPESIMYRKFTTESDVSLSGLVLMETFTYK 598
QY 752 QPWYLSNNEVEICITQGRVLRPRTCPQEVYELMLGCWQREPHRKNKIKIHTLLQNL 811
DB 599 QPWYLSNNEVEICITQGRVLRPRTCPQEVYELMLGCWQREPHRKNKIKIHTLLQNL 658
QY 812 KASPVYLDIIG 822
DB 659 KASPVYLDIIG 669
RESULT 9
Q8WKJ5 PRELIMINARY; PRT; 553 AA.
ID Q8WKJ5
AC Q8WKJ5;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
GN Neurotrophin receptor tyrosine kinase type 2 truncated isoform.
GN Name=NTKR2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N. A.
RX MEDLINE=21656983; PubMed=11798182;
RA Stoilov P., Castren E., Stamm S.;
RT "Analysis of the human TrkB gene genomic organization reveals novel
RT TrkB isoforms, unusual gene length, and splicing mechanism.";
RL Biochem. Biophys. Res. Commun. 290:1054-1065(2002).
RN [2]
RP SEQUENCE FROM N. A.
RA Stoilov P.G., Castren E., Stamm S.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF410901; AAL67967.1; -.
DR HSSP; Q16620; IMMB.
DR GO: GO:0016301; F:kinase activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR Pfam: PF01462; LRRT; 1.
DR SMART: SM00082; LRRT; 1.
DR SMART: SM00013; LRRT; 1.
DR SMART: SM00013; LRRT; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Kinase; Receptor.
SQ SEQUENCE 553 AA; 60993 MW; BD98221B9EB1A6C1 CRC64;
Query Match 64.0%; Score 2826; DB 2; Length 553;
Best Local Similarity 96.9%; Pred. No. 9e-158;
Matches 528; Conservative 1; Mismatches 0; Indels 16; Gaps 1;
QY 1 MSSWIRHNGPAMARLWFCMLVGFMAAFACPTSCSKASRIWCSPPGIVAFPRLEP 60
DB 1 MSSWIRHNGPAMARLWFCMLVGFMAAFACPTSCSKASRIWCSPPGIVAFPRLEP 60
QY 61 NSVDENITETIFIANQRLBITNEDVYAYVGLNLTIVDSGLKFAVHAKAFKXSNLOHI 120
DB 61 NSVDENITETIFIANQRLBITNEDVYAYVGLNLTIVDSGLKFAVHAKAFKXSNLOHI 120
QY 121 NFRPNKLTSLSRKGFRLDLSELILVGNPFTSCSDIMWITLQRAKSSPDODLYCLNES 180
DB 121 NFRPNKLTSLSRKGFRLDLSELILVGNPFTSCSDIMWITLQRAKSSPDODLYCLNES 180
QY 181 SKNIPLANQIPNCGLPANLAPMLTVEGKSTITLSCSVAGDPVPMYMDVGNLVSKIM 240


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DB 181 SKIPLPLANLQIPNCGLPSPALMAAPNLVYBEGSKSTTSSCSVAGDPVPMYMDVGNLVSXKM 240
QY 241 NETSHTGSLRITNVISSDSDGKOISCAVENLVGEDODSVNLTVHFAPTITFLBSPSDH 300
DB 241 NETSHTGSLRITNVISSDSDGKOISCAVENLVGEDODSVNLTVHFAPTITFLBSPSDH 300
QY 301 WCIPFYKGNPKPALQWFFNGALINSEKVICTKHVNTNHEHYGCLQDLPMTMANGDYT 360
DB 301 WCIPFYKGNPKPALQWFFNGALINSEKVICTKHVNTNHEHYGCLQDLPMTMANGDYT 360
QY 361 LIKNEYGKDEKOISAHFMCGPIDDANPNYPVIVEDYGTANDIGDTTNSNEIPST 420
DB 361 LIKNEYGKDEKOISAHFMCGPIDDANPNYPVIVEDYGTANDIGDTTNSNEIPST 420
QY 421 DVTDKTGREHLVYAVVAVVIVASVGFCLVNLFLKLARHSKFGMK----- 465
DB 421 DVTDKTGREHLVYAVVAVVIVASVGFCLVNLFLKLARHSKFGMKDFSWFGFKVSRQG 480
QY 466 -GPASVYSNDDDSAPLHISNGSNTSSSGGPDVAVIGMTKIPVLENPOYRGITNSOL 524
DB 466 -GPASVYSNDDDSAPLHISNGSNTSSSGGPDVAVIGMTKIPVLENPOYRGITNSOL 524
QY 525 KPDTF 529
DB 541 KPDTW 545

RESULT 10
06VNS1
ID 06VNS1 PRELIMINARY; PRT; 825 AA.
AC 06VNS1;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Neurotrophic tyrosine kinase receptor.
GN Name=TrkC;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=14614136; DOI=10.1073/pnas.2336152100;
RA Yamauchi J., Chan Y.R., Shooter E.M.;
RT "Neurotrophin 3 activation of TrkC induces Schwann cell migration
RT through the c-Jun N-terminal kinase pathway."
RL Proc Natl. Acad. Sci. U.S.A. 100:14421-14426(2003).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin
CC receptor subfamily.
CC EMBL: AY336094; AAP94280.1; -.
DB HSP: P08069; IKA.
DR GO: GO:0005615; C:extracellular space; TAS.
DR GO: GO:0016021; C:integral to membrane; TAS.
DR GO: GO:0005515; F:protein binding; IPI.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR011009; kinase_like.
DR InterPro: IPR016111; LRR.
DR InterPro: IPR00483; LRR_Cterm.
DR InterPro: IPR00372; LRR_Nterm.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002011; ReceptTykKinase.
DR InterPro: IPR002290; Ser_Chr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR InterPro: IPR008266; Tyr_kinase_AS.
DR Pfam: PF00047; 1g; 1.
DR Pfam: PF01463; LRNT; 1.
DR Pfam: PF00560; LRR_1; 2.
DR PRINTS: PR00019; LEURICHRPT.

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DR PRINTS: PR00019; TYRKINASE.
DR PRODOM: PD000001; Prot_kinase; 1.
DR SMART: SM00409; IG; 1.
DR SMART: SM00082; LRCT; 1.
DR SMART: SM00013; LRNT; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TykC; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_1; 1.
DR APP-BINDING: Kinase; Phosphorylation; Receptor; Transferase;
KW Transmembrane.
SQ SEQUENCE 825 AA; 92760 MW; 4DE08AB546CC5BD6 CRC64;

Query Match 52.0%; Score 2296; DB 2; Length 825;
Best local similarity 55.0%; Pred. No. 2e-126;
Matches 468; Conservative 107; Mismatches 206; Indels 70; Gaps 16;

QY 10 PAMARL-----GFCWL-VVGFRAAFACPTSCKSASRIWCSDPSPGIVAFRLLEP--- 60
DB 7 PAKCFMRIFLGSVMDYVG---SVLACPANCVCSTELNCRPPDGNL-FLLEGGDS 62
QY 61 -----NSVD-PENITEIFANOKLEIINEDDVEAVVGGRLNLTIVDSGLKFAHKA 110
DB 63 GNSGNASINITIDISRNITSIHLENWRGLHTLAADVMEITYGLQKLTNNSGLRNIOGRA 122
QY 111 FLKSNLIQHINFRNKLTSLSRKPHRLDLSELVGNPFTSCSDIMIKTLQE-AKSP 169
DB 123 FAKNPHLRYNLSNNLTLSMQLPOTLSRELRLEQNFPNGCDDLRMQLMGEQBARL 182
QY 170 DTQDYLCLNESSKNIPLANIQPNCGLPSANLAPLVYBEGSKITLSCVAGDPVPMY 229
DB 183 DSQSLVCISADGSQLPLFRMNISQCLPRTSVSHVNLTVBGNNAVITCNGSGSLPDDVD 242
QY 230 WDVGNLVS-----KHNVEHTGSGSLRITNVISSDSDGKOISCAVENLVGEDODSVNLTVH 264
DB 243 WITYGQISINTQNTNMTNVAHINTLVNVTSEDDGFTLTCAENVVGNASVALTVY 302
QY 285 FAPTITFLBSPSDHDMICPFTVGNPKPALQWFFNGALINSEKVICTKHVNTNHEYH- 343
DB 303 YPRPVSVLVEPRVRLHCHIEFVVRGNPFTLHNLNGOPLRESKII-----HMDYQ 354
QY 344 -----GCLQDLPMTMANGDYTLIAKNEYGKDEKOISAHFMCGPIDDANPNYPDVIV 397
DB 355 EGEVSEGLLFNKPFTYNNNGNYTLIAKNAIGTANQTINGHFLKEP-----FPE--- 402
QY 398 EDVGTANDIGDTTNSNEIPSTDVDTKGRHELSVYAVVIVASVGFCLVNLFL-- 454
DB 403 -----STDFDESASPTPTVTTHKPBBDTFGVSIAGLAFA--CVLLVLFPTMIN 454
QY 455 KLAHRSKFGMGKSPASVYSNDDDSAPLHISNGSNTSSSGGPDVAVIGMTKIPVLENP 514
DB 455 KYGRSKFGMGKGVAVISGEEDSAPLHINHOITTPSSLDADPDVIVIGMTKIPVLENP 514
QY 515 QYRGITNSKPDPTVOHIKRHNIVLKRELGSAGFGKFLAACYNLCPEODKILVAVKTL 574
DB 515 QYFRQGNCHCKPDVYOHIKRDIVLKRELGSAGFGKFLAACYNLSPTDKMLVAVKAL 574
QY 575 KDSADNARKDFHREABILLTLQHEHYKPYGCVYBGDDPLINVEYMGGLNKLFLRAHGP 634
DB 575 KDPFLAARKDFOREABILLTLQHEHYKPYGCVYBGDDPLINVEYMGGLNKLFLRAHGP 634
QY 635 DAVLMAAGNP---PTLTSQMLHIAQVLAAGVYLAASQHFVYRDATRCVGENLTVK 691
DB 635 DAVLIVDGOGRQAKGSLGSQMLHISQVLAASQHFVYRDATRCVGENLTVK 694
QY 692 IGFPGMSRDVYSTDYRVVGHNTMLPIRMPPBSIMYRKFTTESDVSIGVLAWEIFTYGG 751
DB 695 IGFPGMSRDVYSTDYRVVGHNTMLPIRMPPBSIMYRKFTTESDVSIGVLAWEIFTYGG 754
QY 752 QPMYQUSNNEVICITQGRVLAQRPRTCQREYELMLGCMQREBPMRNKINGHTLQNL 811

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Db      755 QPMWQLSTVEICITIGGRVLEPRVCKEYVDWLGCMQREPOORLNITKEIKYILHMLG 814
Qy      812 KASPVYLDILG 822
Db      815 KATPIYDILG 825

RESULT 11
Q080WU0 PRELIMINARY; PRT; 476 AA.
ID Q080WU0
AC Q080WU0
DT 01-JUN-2003 (TRENBLREL 24, Created)
DT 01-MAR-2004 (TRENBLREL 26, last sequence update)
DT 01-MAR-2004 (TRENBLREL 26, last annotation update)
DE Neurotrophic tyrosine kinase, receptor, type 2.
GN Name=Ntrk2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.J., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywnicki M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.U., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Straube R.J.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC052014; AAHS2014.2; -
DR HSP; Q16620; IMWB.
DR MGD; MGI:97384; Ntrk2.
DR GO; GO:0005829; C:cytosol; IDA.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007631; P:feeding behavior; IMP.
DR GO; GO:0019222; P:regulation of metabolism; IMP.
DR GO; GO:0046548; P:retinal rod cell development; IMP.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR000483; IRR_Cterm.
DR InterPro; IPR000372; IRR_Nterm.
DR Pfam; PF01462; LRRT; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00082; LRRT; 1.
DR SMART; SM00013; LRRT; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Kinase; Receptor.
SQ SEQUENCE 476 AA; 53185 MW; 20A8B375BD397ACE CRC64;

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Query Match 51.9%; Score 2292.5; DB 2; Length 476;
Best Local Similarity 89.7%; Pred. No. 1.6e-126;
Matches 418; Conservative 27; Mismatches 20; Indels 1; Gaps 1;

Qy 1 MSSWIRHGPAMARLWGCWLVGFWRAPAFACPTSCCKSASRIMCSPSPGIVAPPRLEP 60
Db 1 MSPWIKHGPAMARLWGCWLVGFWRAPAFACPTSCCKSASRIMCSPSPGIVAPPRLEP 60
Qy 61 NSVDPENITTEIFIANQRLIINEDVYAYVGLNLTIVDSGLKFAVAKPLKSNLQHI 120
Db 61 NSVDPENITTEIFIANQRLIINEDVYAYVGLNLTIVDSGLKFAVAKPLKSNLQHI 120
Qy 121 NPTNKLITSRKPRFLDLSELIVGNPPTSCDIWIKTLQAKSPPTDYLCLNES 180
Db 121 NPTNKLITSRKPRFLDLSELIVGNPPTSCDIWIKTLQAKSPPTDYLCLNES 180
Qy 181 SKNPLANLQIPNCGLSANLAAPNLVVEGSKSTLSCSVAGDPVPMYVGNLVSKM 240
Db 181 SKNPLANLQIPNCGLSANLAAPNLVVEGSKSTLSCSVAGDPVPMYVGNLVSKM 240
Qy 241 NETSHTOGSLRITNISDDSGKQISVAVENLVGEDQDSVNLTVFAPTITLESPTSDDH 300
Db 241 NETSHTOGSLRITNISDDSGKQISVAVENLVGEDQDSVNLTVFAPTITLESPTSDDH 300
Qy 301 WCIPFTVKNPKPALQFNYGAILNESKYICTKHVTNTHRYGCLQIDNPTNNNGDYT 360
Db 301 WCIPFTVKNPKPALQFNYGAILNESKYICTKHVTNTHRYGCLQIDNPTNNNGDYT 360
Qy 361 LIANREYKQEKQISAFPMGPGIDGANPRYEDVIYEDYTAANDIGDTNRSNEIST 420
Db 361 LIANREYKQEKQISAFPMGPGIDGANPRYEDVIYEDYTAANDIGDTNRSNEIST 420
Qy 421 DVTDQREHLSTVAVVAVIVSVGFCLVLMFLKLARSHKFGKMG 466
Db 421 DVTDQREHLSTVAVVAVIVSVGFCLVLMFLKLARSHKFGKMG 466
Db 420 DVTDQREHLSTVAVVAVIVSVGFCLVLMFLKLARSHKFGKMG 465

RESULT 12
TRKC HUMAN
ID TRKC HUMAN STANDARD; PRT; 839 AA.
AC Q16288; Q12827; Q16289.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, last sequence update)
DT 25-OCT-2004 (Rel. 45, last annotation update)
DE NT-3 growth factor receptor precursor (EC 2.7.1.112) (TrkC tyrosine
DE kinase) (Gp145-TrkC) (Trk-C).
GN Name=NTK3; Synonym=TRKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS A, B, C AND D), AND PARTIAL SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=95124473; PubMed=7823156;
RA Shelton D.L., Sutherland J., Gripp J., Camerato T., Armanini M.P.,
RA Phillips H.S., Carroll K., Spencer S.D., Levinson A.D.;
RT "Human trks: molecular cloning, tissue distribution, and expression of
RT extracellular domain immunoadhesins."
RL J. Neurosci. 15:477-491(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS A AND C).
RC TISSUE=Fetal brain;
RX MEDLINE=95104834; PubMed=7806211;
RA McGregor L.M., Baylín S.B., Griffin C.A., Hawkins A.L., Nelkin B.D.;
RT "Molecular cloning of the cDNA for human TrkC (NTRK3), chromosomal
RT assignment, and evidence for a splice variant."
RL Genomics 22:267-272(1994).
CC -1- FUNCTION: Receptor for neurotrophin-3 (NT-3). This is a tyrosine-
CC protein kinase receptor. Known substrates for the trk receptors
CC are SHC1, PI-3 kinase, and PLCG1. The different isoforms do not
CC have identical signaling properties.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

```

CC Tyrosine phosphate.
 CC -1- SUBUNIT: Exists in a dynamic equilibrium between monomeric (low
 CC affinity) and dimeric (high affinity) structures (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=4;
 CC Comment-Additional isoforms seem to exist;
 CC Name=A;
 CC IsoId=Q16288-1; Sequence=Displayed;
 CC Name=B;
 CC IsoId=Q16288-2; Sequence=VSP_002925, VSP_002926;
 CC Name=C;
 CC IsoId=Q16288-3; Sequence=VSP_002927;
 CC Name=D;
 CC IsoId=Q16288-4; Sequence=VSP_002924;
 CC -1- TISSUE SPECIFICITY: Widely expressed, mainly in the nervous
 CC tissue. The isoform B is expressed in a relatively large amount in
 CC the adult brain comparatively to fetal brain.
 CC -1- PPM: Ligand-mediated auto-phosphorylation.
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. Insulin
 CC receptor subfamily.
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 2 leucine-rich (LRR) repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL: S76475; AAB3111.1; -;
 CC EMBL: S76476; AAB3112.1; -;
 CC EMBL: U05012; AAA75374.1; -;
 CC PIR: I73632; I73632.
 CC PIR: I73633; I73633.
 CC PDB: 1WVC; X-ray; A=297-414.
 CC Genew: HGNC:8033; NTRK3.
 CC H-InvDB: HIX0012549; -;
 CC MIM: 191316; -;
 CC DR GO: GO:0005887; C:intracellular plasma membrane; TAS.
 CC DR GO: GO:0005016; P:neurotrophin TRK receptor activity; TAS.
 CC DR GO: GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; TAS.
 CC DR InterPro: IPR003599; Ig.
 CC DR InterPro: IPR007110; Ig-like.
 CC DR InterPro: IPR011009; Kinase_like.
 CC DR InterPro: IPR001611; LRR.
 CC DR InterPro: IPR000483; LRR_Cterm.
 CC DR InterPro: IPR000372; LRR_Nterm.
 CC DR InterPro: IPR000719; Prot_Kinase.
 CC DR InterPro: IPR002011; ReceptTyKinsII.
 CC DR InterPro: IPR001245; Tyr_Kinase.
 CC DR InterPro: IPR008266; Tyr_Kinase_AS.
 CC Pfam: PF00047; Ig; 1.
 CC Pfam: PF00560; LRR; 2.
 CC Pfam: PF01462; LRRNT; 1.
 CC Pfam: PF00069; Kinase; 1.
 CC PRINTS: PR00019; LEURICHRPT.
 CC PRINTS: PR00109; TYRKINASE.
 CC PRODOM: PD000001; Prot_Kinase; 1.
 CC SMART: SM00409; IG; 1.
 CC SMART: SM00082; LRRCT; 1.
 CC SMART: SM00013; LRRNT; 1.
 CC SMART: SM00219; TYRK; 1.
 CC PROSITE: PS50835; IG_LIKE; 1.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 CC PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 CC PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
 CC 3D-structure: Alternative splicing; ATP-binding;
 CC Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
 CC Leucine-rich repeat; Neurogenesis; Phosphorylation; Receptor; Repeat;

KW Signal; Transferase; Transmembrane; Tyrosine-protein kinase.
 FT SIGNAL 1 31
 FT CHAIN 32 839
 FT DOMAIN 32 429
 FT TRANSMEM 430 453
 FT DOMAIN 454 839
 FT REPEAT 102 125
 FT REPEAT 126 149
 FT DOMAIN 210 300
 FT DOMAIN 309 382
 FT DOMAIN 538 839
 FT NP_BIND 544 552
 FT BINDING 572 572
 FT ACT_SITE 679 679
 FT MOD_RES 516 516
 FT MOD_RES 705 705
 FT MOD_RES 709 709
 FT MOD_RES 710 710
 FT MOD_RES 834 834
 FT SITE 834 834
 FT CARBOHYD 72 72
 FT CARBOHYD 79 79
 FT CARBOHYD 133 133
 FT CARBOHYD 163 163
 FT CARBOHYD 203 203
 FT CARBOHYD 218 218
 FT CARBOHYD 232 232
 FT CARBOHYD 259 259
 FT CARBOHYD 267 267
 FT CARBOHYD 272 272
 FT CARBOHYD 294 294
 FT CARBOHYD 375 375
 FT CARBOHYD 388 388
 FT CARBOHYD 402 410
 FT VARSPPLIC 529 612
 FT VARSPPLIC 613 839
 FT VARSPPLIC 712 725
 FT CONFLICT 70 70
 FT CONFLICT 635 635
 FT STRAND 318 326
 FT STRAND 332 337
 FT TURN 338 339
 FT STRAND 340 341
 FT STRAND 348 354
 FT STRAND 358 366
 FT HELIX 370 372
 FT STRAND 374 382
 FT TURN 383 384
 FT STRAND 385 393
 SQ SEQUENCE 839 AA; 94455 MW; 86D965A503B4DDD CRC64;
 Query Match 51.5%; Score 2277; DB 1; Length 839;
 Best Local Similarity 53.7%; Pred. No. 2.6e-125;
 Matches 467; Conservative 110; Mismatches 199; Indels 94; Gaps 18;
 Oy PAMARLM-----GFCWL-VVGFMAAPACPTSCCKSARIMCSPSPGIVAFPLEP---60
 Db 7 PAKSFRIRILSLGSVMDYVG---SVLACPRANCVCSTETINCRPDDONL-FILLBOGDS 62

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QY 61 -----NSVD-PENITRIFIANQRLKELINEDVEAYVGLNLTIVDSGLKFWAHKA 110
DB 63 GNSNGNANINITDTSRNTSITHIENMRSILHTLANVDEMLYGLQKLTIKNSGLRSIOGRA 122
QY 111 FLKSNLQHINFTFNKLTSLSRKHFRHLDSELLVGNPFTGSCDIMWIKTLQF-AASSP 169
DB 123 FAKSPHRLRYINLSSNRLTTLTSLWOLFQTLSTRELQLEONFFGSCDIRMWQMOQGAKL 182
QY 170 DTODLYCLANSSKNIPANLQIPNCGP.SANLAAPNLVTEGKSTLSCVAGDPVPMY 229
DB 183 NSQNLTCINADGSLPLFRANITSCDLPESVSHVNLTVREGDNAVITTCNGSSPLDPVD 242
QY 230 WDVGNLVS-----KHNETSHQSLRITNISSDSGKOISCVANLVGEODQSVNLTVH 284
DB 243 WLVTLGQSIHTHQNLMTWNVHAILNLTVNTSLEDNGFTLCLIAENVGNMNAVALTVY 302
QY 285 FAPITITLESPTSHHMCIPFTVGNKPKALQWYNGALINESKYICTKHVHTVTEYH- 343
DB 303 YPPRVVSLLEBEURLLEHCIEFVVGNGNPPTLHMLHNOPLRESKTI-----HVEYQ 354
QY 344 -----GCLQLDNPTNNGNDYTLIAKNEVGKDEKOISAHFMWPGIDDGANPNYPD--- 394
DB 355 EGEISECCLFNKRTHTNNGVTLIAKNPLGTANQTLNGHFLKEP-----FPESSTD 405
QY 395 --VLEDYGTAAANDIGDTYKRSNEIPSTDVDTKGRHLSYAVAVIASVVGFC-LVMTL 451
DB 406 NFLIFDEV-----SPTPLITVTHKPEEDTFGSIAVGLAFA--CVLVLVL 449
QY 452 FL--KLARSKFKMGKPAVYSNDSDASPLHIHISNGSNTSSSEGGPDVITIGMTIP 509
DB 450 FVMINKYGRSKFKMGKPAVAVISGEEDSASPLHIHINIGITTPSSILDAGPDTVVIGMRIP 509
QY 510 VIENPOYFGITNSQKPTFVQHTKRNHYVAKRELGSAGPKVLAECYNLCEPDOKTIV 569
DB 510 VIENPOYFGROCHNKHEDTIVQHKRDIVAKRELGSAGPKVLAECYNLSPYKQVLV 569
QY 570 AVKTLKASDNARKDFRREAEELTNLOHEHIVKEFYGVCEBGPLIMVEYKHSGLNKL 629
DB 570 AVAKLXOPTLARKDFRREAEELTNLOHEHIVKEFYGVCEBGPLIMVEYKHSGLNKL 629
QY 630 RAHGPDVLAABGNP---PTELTSQMLHIAQOIAAGNVYIASGHFVHRLATNCLVGE 686
DB 630 RAHGPDAMIIVDQGPRAKSELGSLQMLHIASQIASGVYIASGHFVHRLATNCLVGA 689
QY 687 NLVYKIDGFGMSRNVYSTDYR-----VGGHMLDIRMPPESIVYRKFTT 732
DB 690 NLVYKIDGFGMSRNVYSTDYRFLPNPBGNDPCIVCEVGHMTLIRMPPEISIVYRKFTT 749
QY 733 ESDVWSLGVVLMELFTYGGKOPWYOLSNNEVEICTOGSVLQRPRTCPQEVYELMLGCMOR 792
DB 750 ESDVWSGCVILMEIFTYGGKOPWYOLSNNEVEICTOGSVLQRPRTCPQEVYELMLGCMOR 809
QY 793 EPHMRKNIKGIHTLLQMLANASPYVLDILG 822
DB 810 EPGORLNKEIKYILHIALGKATPIYLDILG 839

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RA Ichaso N., Rodriguez R., Martin-Zanca D., Gonzalez-Sarmiento R.;
RT "Genomic characterization of the human trkC gene.";
RL Oncogene 17:1871-1875(1998).
CC -1- CATALYTIC ACTIVITY. ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- Similarity: Belongs to the Tyr family of protein kinases. Insulin
CC receptor subfamily.
DR EMBL; AJ224521; CA112029.1; -.
DR EMBL; AJ224522; CA112029.1; JOINED.
DR EMBL; AJ224524; CA112029.1; JOINED.
DR EMBL; AJ224523; CA112029.1; JOINED.
DR EMBL; AJ224527; CA112029.1; JOINED.
DR EMBL; AJ224529; CA112029.1; JOINED.
DR EMBL; AJ224531; CA112029.1; JOINED.
DR EMBL; AJ224533; CA112029.1; JOINED.
DR EMBL; AJ224535; CA112029.1; JOINED.
DR EMBL; AJ224534; CA112029.1; JOINED.
DR EMBL; AJ224532; CA112029.1; JOINED.
DR EMBL; AJ224530; CA112029.1; JOINED.
DR EMBL; AJ224528; CA112029.1; JOINED.
DR EMBL; AJ224526; CA112029.1; JOINED.
DR EMBL; AJ224525; CA112029.1; JOINED.
DR HSSE; Q16288; IWC.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002011; Recepttyrknsit.
DR InterPro; IPR001245; Tyrc_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF01462; LRRNT; 1.
DR Pfam; PF00560; LRR_1; 2.
DR PRINTS; PR00019; LRRICHRPT.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
KW ATP-binding; Kinase; Phosphorylation; Receptor; Transferase;
KW Transmembrane; Tyrosine-protein kinase.
SQ SEQUENCE 839 AA; 94427 MW; 7FE8846830083C08 CRC64;

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Query Match 51.5%; Score 2277; DB 2; Length 839;
Best Local Similarity 53.7%; Pred. No. 2,6e-125;
Matches 467; Conservative 110; Mismatches 199; Indels 94; Gaps 18;

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QY 10 PAMARLM-----GFCWL-VGFWRAAPACTSCKCSASRIWCSDPSPGIVAFPLLP-- 60
DB 7 PAKCSFWRIPLGSLVMDVVG---SVLACPAACVCSKTEINCRAPDDGNTL-FPLLEGDS 62
QY 61 -----NSVD-PENITRIFIANQRLKELINEDVEAYVGLNLTIVDSGLKFWAHKA 110
DB 63 GNSNGNANINITDTSRNTSITHIENMRSILHTLANVDEMLYGLQKLTIKNSGLRSIOGRA 122
QY 111 FLKSNLQHINFTFNKLTSLSRKHFRHLDSELLVGNPFTGSCDIMWIKTLQF-AASSP 169

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Db 123 FAKPHRIYNTLSSNRLTITLSMQLFQTLISRELQLEQNFNCSDIRFMQLNOEGEAKL 182
Qy 170 DTODLYCLNNESSKNIPLANDIIPNCGIPSANLAPNLTVEGKSTLSCVAGDPVPMY 229
Db 183 NSQNLVCYNADGSQLPFRMNISQCDLPEISVSHVNLTVBGNDAVATLCKSGSGPLPDDV 242
Qy 230 WDVGNLVLS-----KHNETSHTGSLRITWISSDSKQISCAVAKNLVGEDOSVNLTVH 264
Db 243 WIVTGLQSIINTHQTNLMTWVNHAINLTVLVNTSDEPNFTLTCLAEVNGSMNSVALTVY 302
Qy 285 FAPTITLESPTSDHMCIPFTVYKGNPKPALOMFYNGALINSEKYICTKLHVTHTYH- 343
Db 303 YPRVNVLSERBELRLHCIFEVVRGNRPPTLHMLHNGOPLRESKLT-----HZZYQ 354
Qy 344 -----GCLQDLPFTANNGDYTLIAKNEYKQEKQISAHFMWPGIDGANPNYPD--- 394
Db 355 EGEISECCLFENKPTHTYNNNGYTLIAKNPGLTANQTINGHFLKRP-----FPESTD 405
Qy 395 --VIEYEGYRANNDIGTTRNSNEIPSTDTDKTGRHLSVYAVVAVASVVGFC-LIVML 451
Db 406 NFLIFDEV-----SPTPIYTHKPEEDTFGVSJAVGLAARA--CVLLVLV 449
Qy 452 FLU--KLARSKFGMKGPASVYISNDSDASPLHHISGNSNTPSSBEGGPPAVIIGMTKIP 509
Db 450 FVMIKTYGRSKFGMKGPVAVISGEBSASPLHHINHGITTSSLDGDPPTVVIAMTRIP 509
Qy 510 VIEBNPOYFGITNSQLKPDPTVOHAKRHNYLKRLEGAGAGKVLAECCYLCPRODKILV 569
Db 510 VIEBNPOYFGQNGHCHKPDYQHKRDYVLRKELGSGAGKGVLABCYNLSPFKDMGLV 569
Qy 570 AVTKLXASDNARKDFRREBELNLNLOHEHVKFYGVCEBDDPLIMFETMKHGLDKFL 629
Db 570 AVVALKOPTLAARDFORRELLNLNLOHEHVKFYGVCGDDPLIMFETMKHGLDKFL 629
Qy 630 RAHGPDVLAEGNP---PTELTSOMLHIAQOIAAGVNYLASOFHARDLATRNCVGS 686
Db 630 RAHGPDVLAEGNP---PTELTSOMLHIAQOIAAGVNYLASOFHARDLATRNCVGS 686
Qy 687 NLVVKIDFGMSRDVYSTDYR-----VGHTMLPIRMMPESIMYRKFTT 732
Db 690 NLVVKIDFGMSRDVYSTDYR-----VGHTMLPIRMMPESIMYRKFTT 749
Qy 733 ESDVMSIGVNLMBIFTYGKOPWYOLSNNEVEICTQGRVLORPTECOEYELMLGCMOR 792
Db 750 ESDVMSIGVNLMBIFTYGKOPWYOLSNNEVEICTQGRVLORPTECOEYELMLGCMOR 809
Qy 793 BPHMRKNIKGHTLLOMLAKSPVYLDITG 822
Db 810 BPOORLNKIKETIKLHAKGKATPYLDITG 839

RESULT 14
TRKC_CHICK STANDARD; PRT; 827 AA.
AC Q91044; Q91011; Q92022;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE NT-3 growth factor receptor precursor (BC 2.7.1.112) (Trkc tyrosine
kinase) (Trk-C).
GN Name=TRKC;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
OX 11
RN SEQUENCE FROM N.A. (ISOFORMS ALPHA-FL, ALPHA-KT, ALPHA-KD, BETA-KD AND
RP KI25).
RC TISSUE=Embryonic brain;
RX MEDLINE=94338700; PubMed=8060621; DOI=10.1016/0896-6273(94)90360-3;
RA Garner A.S., Large T.H.;
RT "Isoforms of the avian Trkc receptor: a novel kinase insertion

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RT dissociates transformation and process outgrowth from survival."
RL Neuron 13:457-472(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA/FL AND TRKC-3).
RX MEDLINE=93359043; PubMed=8394830; DOI=10.1016/0014-5793(93)80216-H;
RA Okazawa H., Kamei M., Kanazawa I.;
RT "Molecular cloning and expression of a novel truncated form of chicken
RL trkC."
RL FEBS Lett. 329:171-177(1993).
RN [3]
RP SEQUENCE OF 378-513 FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=94084905; PubMed=8261614; DOI=10.1016/0165-3806(93)90028-9;
RA Williams R., Backstrom A., Ebdanal T., Hallbook F.;
RT "Molecular cloning and cellular localization of trkC in the chicken
RL embryo."
RL Brain Res. Dev. Brain Res. 75:235-252(1993).
CC -1 FUNCTION: Receptor for neurotrophin-3 (NT-3). This is a tyrosine-
protein kinase receptor. Known substrates for the trk receptors
are SHC1, PI-3 kinase and PLCG1. The RT and KD isoforms fail to
stimulate transformation, process outgrowth or survival. Isoform
KI25 exhibits tyrosine phosphorylation in the absence of ligand
and is unable to mediate survival of neuronal cells.
CC -1 CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
tyrosine phosphate.
CC -1 SUBUNIT: Exists in a dynamic equilibrium between monomeric (low
affinity) and dimeric (high affinity) structures.
CC -1 SUBCELLULAR LOCATION: Type I membrane protein.
CC -1 ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=6;
Comment=Additional isoforms seem to exist;
Name=Alpha-FL;
IsoId=Q91044-1; Sequence=Displayed;
CC Name=Alpha-KT;
IsoId=Q91044-2; Sequence=VSP_002943; VSP_002944;
CC Name=Alpha-KD;
IsoId=Q91044-3; Sequence=VSP_002939; VSP_002940;
CC Name=Beta-KD;
IsoId=Q91044-4; Sequence=VSP_002938; VSP_002939; VSP_002940;
CC Name=TRKC-3;
IsoId=Q91044-5; Sequence=VSP_002941; VSP_002942;
CC Name=KI25;
IsoId=Q91044-6; Sequence=VSP_002945;
CC -1 DEVELOPMENTAL STAGE: Expression occurs in the embryonal day 2 (E2)
embryo with increasing levels later in development. In the E9
embryo highest levels are found in brain and spinal cord with
intermediate levels in eye, heart, gut and muscle. Low levels are
found in kidney, liver, skin and yolk sac.
CC -1 PTM: Ligand-mediated auto-phosphorylation (By similarity).
CC -1 SIMILARITY: Belongs to the tyr protein kinase family. Insulin
receptor subfamily.
CC -1 SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -1 SIMILARITY: Contains 2 leucine-rich (LRR) repeats.
CC -1 CAUTION: The additional kinase-deleted isoform TRKC-3 which
replaces the kinase domain with 19 AA instead of 39 in the isoform
alpha-KD results from a frameshift.
CC -----
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or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; S74248; AABJ1699.1; -
DR EMBL; X59669; CAA42202.1; -
DR EMBL; Z30091; CAA82907.1; -
DR PIR; I51222; I51222.
DR PIR; I51259; I51259.
DR PIR; S35695; S35695.
DR HSBP; Q16288; IWC.
DR InterPro; IPR003599; Ig.

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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR011009; Kinase-like.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002011; ReceptLTKinsII.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; IPR008266; Tyr_kinase_AS.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00560; LRR; 2.
DR Pfam; PF01462; LRRNT; 1.
DR Pfam; PF00069; Primase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00082; LRCT; 1.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
DR Alternative splicing; ATP-binding; Glycoprotein;
KW Immunoglobulin domain; leucine-rich repeat; Neurogenesis;
KW Phosphorylation; Receptor; Repeat; Signal; Transferase; Transmembrane;
KW Tyrosine-protein kinase.
KM TYROSINE-protein kinase.
FT SIGNAL 1 31 By similarity.
FT CHAIN 32 827 NT-3 growth factor receptor.
FT DOMAIN 32 430 Extracellular (Potential).
FT TRANSSEM 431 455 Potential.
FT DOMAIN 456 827 Cytoplasmic (Potential).
FT REPEAT 102 125 LRR 1.
FT REPEAT 126 149 LRR 2.
FT DOMAIN 210 300 Ig-like C2-type 1.
FT DOMAIN 319 382 Ig-like C2-type 2.
FT DOMAIN 540 812 Protein kinase.
FT NP BIND 546 554 ATP (By similarity).
FT BINDING 574 574 ATP (By similarity).
FT ACT_SITE 681 681 Proton acceptor (By similarity).
FT MOD_RES 518 518 Phosphotyrosine (by autocatalysis) (By similarity).
FT MOD_RES 707 707 Phosphotyrosine (by autocatalysis) (By similarity).
FT MOD_RES 711 711 Phosphotyrosine (by autocatalysis) (By similarity).
FT MOD_RES 712 712 Phosphotyrosine (by autocatalysis) (By similarity).
FT MOD_RES 822 822 Phosphotyrosine (by autocatalysis) (By similarity).
FT SITE 518 518 Interaction with SHC1 (By similarity).
FT SITE 822 822 Interaction with PLC-gamma-1 (By similarity).
FT CARBOHYD 62 68 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 72 72 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 79 79 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 163 163 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 203 203 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 218 218 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 232 232 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 259 259 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 267 267 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 272 272 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 294 294 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 375 375 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 388 388 N-linked (GlcNAc...) (Potential).
FT VASPLIC 1 98 Missing (in isoform Beta-KD).
FT VASPLIC 581 619 /FtId=VSP_002938.
FT VASPLIC 581 619 LAARKDQREAEELTNLOHEHIVKRYGVCGGDELIMWF
-> CPEITMLNPISLPGHCKPLNGITVEDVSVFSGKRHG
F (in isoform Alpha-KD and isoform Beta-KD).

FT FT VASPLIC 620 827 /FtId=VSP_002939.
FT FT VASPLIC 581 599 Missing (in isoform Alpha-KD and isoform Beta-KD).
FT FT VASPLIC 600 827 /FtId=VSP_002940.
FT FT VASPLIC 633 664 LAARKDQREAEELTNLOH -> CPEITMLNPISLPGHCQT
S (in isoform TRKC-3).
FT FT VASPLIC 600 827 /FtId=VSP_002941.
FT FT VASPLIC 633 664 Missing (in isoform TRKC-3).
FT FT VASPLIC 665 827 /FtId=VSP_002942.
FT FT VASPLIC 713 713 /FtId=VSP_002943.
FT FT VASPLIC 713 713 /FtId=VSP_002944.
FT FT VASPLIC 713 713 R -> RSGPRKGLSTAMQGNRLAPPAAT (in isoform KI25).
FT FT VASPLIC 1 39 /FtId=VSP_002945.
FT FT VASPLIC 124 124 MDVSLCTKCTFMVVFLLMSIWGDYLSVACPNCLCS
CONFLICT 378 378 -> MHFICWRIFASDRKLVLP (in Ref. 2).
FT FT VASPLIC 481 496 A -> G (in Ref. 2).
FT FT VASPLIC 481 496 I -> P (in Ref. 3).
FT FT VASPLIC 795 795 SPLHINHGITTPESL -> ATRHSTDTREVT (in Ref. 2).
FT FT VASPLIC 827 AA; 93180 MW; AB97373113DCB28A CRC64;
SQ SEQUENCE 827 AA; 93180 MW; AB97373113DCB28A CRC64;
Query Match 51.5%; Score 2275; DB 1; Length 827;
Best Local Similarity 54.3%; Pred. No. 3,46-125;
Matches 463; Conservative 114; Mismatches 204; Indels 72; Gaps 17;
QY 10 PAMARLGG--FCWLVG-FWRAPACPTSCSKASRIWCSDPSGIVAPFLPEP----- 60
Db 7 PTKCTFWRVFLMSIWGDYLSVACPNCLCSKTIDNCKKDDGNL-FLLLEGGDSSGS 65
QY 61 -----NSVD-PENITEIFIANQRLIEINEDVEAYVGLNLTIVDSGLKFAVAKFLK 113
Db 66 NGNTSINITISRNITSIHIEIEMWNLQTLNAVDELYTGLRILIRNSGLNIOPRAAK 125
QY 114 NSNQHINFRNKLTSRKGRFLDSELLVNPPTCCGDIWMITLQD-AASSPTQ 172
Db 126 NPHLRVYIDLSGNRLTTLTSMQLFQTLRLFLRLLENPNRSCDIDIMQIMQKGRANLQSQ 185
QY 173 DLYCLNASSKNIPLANQIPNCGSPSANLAPNLTVREGSKITLCSVAGDPVPMWVDV 232
Db 186 QLRHMLDPAVILIRANNTIQCDPEISVSHVNLTVREGNAVITTCGSSGPLDQDVT 245
QY 233 GNIVS-----KMNETHSTGSLRITNISDDSGQISCVANLVGDDODSVNLTVFAP 287
Db 246 ADHSINWHTQNNLWTVVHAINLTVNVTSEBDFLLTCLAEVNVGMSNVLLTVVYP 305
QY 288 TITLSEPTSDHMCIFPTVYKGNPKPALOWFYNGAAILNESKYICTKIHVNTHTYH---- 343
Db 306 RILTLSEPVVLEHCIAFAVGNPAPFLHMLHNCQVLRTEIIL-----HMEFYQGE 357
QY 344 ---GCLDNPPTMNNNGDYTLIAKNEYGKDEKQISAFPMGPGIDDGNPVYPD-----V 395
Db 358 VBSCLTFNKPETHYNNNGYITVATNQASANQITKGFLEKP-----FPESTDNFV 408
QY 396 IYEDYGTANDIDGTTTNRSEIPESTDVTDKTRHLSVYAVAVVIVASVGF-C-LVMFL 454
Db 409 SIGDY-----EVSPT-----PRTVTHKREBDTPGVSAIVGLAFA-CVLLVLPIM 454
QY 455 --KLARSKGKMGKPAVISNDDSDAPLHISNGSWTPSSBGGPDPAVITGKTIPIYB 512
Db 455 INKYGRRSKGKMGKPAVISNDDSDAPLHISNGSWTPSSBGGPDPAVITGKTIPIYB 514
QY 513 NPQVFGITNSQLKPDFTVOHVKHNIYVKREIGARGKVFACVNYLCPEDKILVAVK 572
Db 515 NPQVFGITNSQLKPDFTVOHVKHNIYVKREIGARGKVFACVNYLCPEDKILVAVK 574
QY 573 TLKQASNAKQDFIREAEELTNLOHEHIVKRYGVCGGDELIMWF 632

Db 575 ALADPTLAARKDQFQREABLTNLQHEHIVKFGVCGDPLIMVFYMKHGDLNKFIRAH 634
 QY 633 GPDVAIIMAGNPN--PTLETQOSQMLHIAQOIAGMVTIASQHPVHRDLATRNCLVGENLL 689
 Db 635 GPDAMIIVDQGPQAKGELGISQMLHIASQIASGMVTIASQHPVHRDLATRNCLVGENLL 694
 QY 690 VKIGDPMGMSDVSVDYVYRGHGMPLPIRMMPRESIVYRKPTTESDWSIGVYLWELFTY 749
 Db 695 VKIGDPMGMSDVSVDYVYRGHGMPLPIRMMPRESIVYRKPTTESDWSIGVYLWELFTY 754
 QY 750 GKQPMYQISNNVEICTQGRVLRPTCPQEVVELMGVQMRSPHNRKNIKGHTLTON 809
 Db 755 GKQPMYQISNNVEICTQGRVLRPTCPQEVVELMGVQMRSPHNRKNIKGHTLTON 814
 QY 810 LAKASPYLIDLG 822
 Db 815 LKATPTIYDILIG 827

RESULT 15
 TRKC_RAT STANDARD; PRT, 864 AA.
 AC 003351;
 DT 01-OCT-1993 (Ref. 27, Created)
 DT 01-FEB-1994 (Ref. 28, Last sequence update)
 DT 05-JUL-2004 (Ref. 44, Last annotation update)
 DE NT-3 growth factor receptor precursor (BC 2.7.1.112) (TRKC tyrosine kinase) (GP145-TRKC) (TRK-C).
 GN Name=TrkC; Synonyms=TrkC;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RX [1]
 RP SEQUENCE FROM N.A. (ISOFORM TRKC).
 RX MEDLINE=33140933; PubMed=1488112; DOI=10.1016/0306-4522(92)90292-A;
 RA Merllo J.P., Ernforts P., Jaber M., Persson H.;
 RT "Molecular cloning of rat trkc and distribution of cells expressing messenger RNAs for members of the trk family in the rat central nervous system.";
 RT Neuroscience 51:513-532 (1992).
 RL Neuron 10:963-974 (1993).
 RN [2]
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=33264091; PubMed=8494647; DOI=10.1016/0896-6273(93)90211-9;
 RA Valenzuela D.M., Maisonnier P.C., Glaes D.J., Rojas R., Munoz L., Kong Y., Gies D.R., Stitt T.N., Ip N.Y., Yancopoulos G.D.;
 RT "Alternative forms of rat TrkC with different functional capabilities.";
 RT Neuron 10:963-974 (1993).
 RN [3]
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain cortex, and Hippocampus;
 RX MEDLINE=33264092; PubMed=8494648; DOI=10.1016/0896-6273(93)90212-A;
 RA Teoulas P., Soppet D., Bascand E., Tessarollo L., Mendoza-Ramirez J.-L., Rosenthal A., Nikolic K., Parada L.F.;
 RT "The rat trkc locus encodes multiple neurogenic receptors that exhibit differential response to neurotrophin-3 in PC12 cells.";
 RT Neuron 10:975-990 (1993).
 RL -1- FUNCTION: Receptor for neurotrophin-3 (NTF3). This is a tyrosine-protein kinase receptor. Known substrates for the Trk receptors are SHC1, PI-3 kinase, and PLCG1. TrkC isoforms containing insertions within the kinase domain can autophosphorylate in response to NTF-3, but cannot mediate downstream phenotypic responses.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
 CC -1- SUBUNIT: Exists in a dynamic equilibrium between monomeric (low affinity) and dimeric (high affinity) structures.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=8;
 CC Comment=Additional isoforms seem to exist;

CC Name=K139; Synonyms=TRKC(K139), TRKC-39;
 CC IsoId=Q03351-1; Sequence=Displayed;
 CC Name=TRKC;
 CC IsoId=Q03351-2; Sequence=VSP_002936, VSP_002937;
 CC Name=K14; Synonyms=TRKC(K14), TRKC-14;
 CC IsoId=Q03351-3; Sequence=VSP_002936;
 CC Name=K125; Synonyms=TRKC-25;
 CC IsoId=Q03351-4; Sequence=VSP_002937;
 CC Name=IC158; Synonyms=TRKC(IC158), TRKCTK-;
 CC IsoId=Q03351-5; Sequence=VSP_002934, VSP_002935;
 CC Name=IC143; Synonyms=TRKC(IC143);
 CC IsoId=Q03351-6; Sequence=VSP_002932, VSP_002933;
 CC Name=IC113; Synonyms=TRKC(IC113);
 CC IsoId=Q03351-7; Sequence=VSP_002930, VSP_002931;
 CC Name=IC108; Synonyms=TRKC(IC108);
 CC IsoId=Q03351-8; Sequence=VSP_002928, VSP_002929;
 CC -1- TISSUE SPECIFICITY: Widely expressed, mainly in the nervous tissue.
 CC -1- PTM: Ligand-mediated auto-phosphorylation.
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. Insulin receptor subfamily.
 CC -1- SIMILARITY: Contains 2 leucine-rich (LRR) repeats.
 CC -----
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 CC -----
 CC EMBL: L03813; AAA42285.1; -
 CC EMBL: L14445; AAA42282.1; -
 CC EMBL: L14446; AAA42283.1; -
 CC EMBL: L14447; AAA42284.1; -
 CC EMBL: S60953; AAB26714.2; -
 CC EMBL: S62924; AAB26716.2; -
 CC EMBL: S62933; AAB26715.2; -
 CC HSP: Q16288; IWC.
 CC RGD: 3214; Ntrk3.
 CC InterPro: IPR003599; Ig.
 CC InterPro: IPR007110; Ig-like.
 CC InterPro: IPR011009; Kinase_like.
 CC InterPro: IPR001611; LRR.
 CC InterPro: IPR000483; LRR_Cterm.
 CC InterPro: IPR000372; LRR_Nterm.
 CC InterPro: IPR002011; ReceptTykkinet.
 CC InterPro: IPR001245; Tyr_kinase.
 CC InterPro: IPR008266; Tyr_pkinase_AS.
 CC Pfam: PF00047; Ig_1.
 CC Pfam: PF00560; LRR_2.
 CC Pfam: PF01462; LRRNT_1.
 CC Pfam: PF00069; Kinase_1.
 CC PRINTS: PR00019; LRRICHRPT.
 CC PRODOM: PD000001; TYRKINASE.
 CC SMART: SM00409; Ig_1.
 CC SMART: SM00082; LRRCT_1.
 CC SMART: SM00013; LRRNT_1.
 CC SMART: SM00219; Tyrc; 1.
 CC PROSITE: PS50835; IG LIKE_1.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
 CC PROSITE: PS50011; PROTEIN_KINASE_DOM_1.
 CC PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
 CC PROSITE: PS00239; RECEPTOR_TYR_KIN_1; 1.
 CC Alternative splicing; ATP-Binding; Glycoprotein;
 CC Immunoglobulin domain; Leucine-rich repeat; Neurogenesis;
 CC Phosphorylation; Receptor; Repeat; Signal; Transferrase; Transmembrane;
 CC Tyrosine-protein kinase.
 CC SIGNAL 1 31
 CC CHAIN 32 864 By similarity.
 CC FT NT-3 growth factor receptor.

```

FT DOMAIN 32 429 Extracellular (Potential).
FT TRANSLEM 430 453 Potential.
FT DOMAIN 454 864 Cytoplasmic (Potential).
FT REPEAT 102 125 LRR 1.
FT REPEAT 126 149 LRR 2.
FT DOMAIN 210 300 Ig-like C2-type 1.
FT DOMAIN 309 382 Ig-like C2-type 2.
FT DOMAIN 538 853 Protein kinase.
FT NP BIND 544 552 ATP (By similarity).
FT BINDING 572 572 ATP (By similarity).
FT ACT SITE 679 679 Proton acceptor (By similarity).
FT MOD_RES 516 516 Phosphotyrosine (by autocatalysis) (By similarity).
FT MOD_RES 705 705 Phosphotyrosine (by autocatalysis) (By similarity).
FT MOD_RES 709 709 Phosphotyrosine (by autocatalysis) (By similarity).
FT MOD_RES 710 710 Phosphotyrosine (by autocatalysis) (By similarity).
FT MOD_RES 859 859 Phosphotyrosine (by autocatalysis) (By similarity).
FT SITE 516 516 Interaction with SHC1 (By similarity).
FT SITE 859 859 Interaction with PLC-gamma-1 (By similarity).
FT CARBOHYD 68 68 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 72 72 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 79 79 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 133 133 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 163 163 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 203 203 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 218 218 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 232 232 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 259 259 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 267 267 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 272 272 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 294 294 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 375 375 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 388 388 N-linked (GlcNAc... ) (Potential).
FT VARSPLIC 529 562 YVOHKKRDYTLKRELGEAGKFLAEVCYNLSPTKDKM IEGFAYGKRYVMVMSVHCPCWFRFGLEML (in isoform IC108).
FT VARSPLIC 563 864 /FTid=VSP_002928. Missing (in isoform IC108).
FT VARSPLIC 529 567 /FTid=VSP_002929. YVOHKKRDYTLKRELGEAGKFLAEVCYNLSPTKDKM -> CFRIMENPISLSGHSKPLNNGIYVEDVNVYFSKGRHS F (in isoform IC113).
FT VARSPLIC 568 864 /FTid=VSP_002930. Missing (in isoform IC113).
FT VARSPLIC 529 597 /FTid=VSP_002931. YVOHKKRDYTLKRELGEAGKFLAEVCYNLSPTKDKM AVKALKDPTLARKDFOREBELTNLOH -> WFSNIDNH GILNLKONRDLVPSHTYIEEPVQSGDVSPSHGELLP LTLSEVKKPLPLVLIKT (in isoform IC143).
FT VARSPLIC 598 864 /FTid=VSP_002932. Missing (in isoform IC143).
FT VARSPLIC 529 612 /FTid=VSP_002933. YVOHKKRDYTLKRELGEAGKFLAEVCYNLSPTKDKM AVKALKDPTLARKDFOREBELTNLOHHEHIVKRYGCGDG DP -> WFSNIDNHGILNLKONRDLVPSHTYIEEPVQSGDVSPSHGELLPISLSGHSKPLNNGIYVEDVNVY FSKGRHGF (in isoform IC158).
FT VARSPLIC 613 864 /FTid=VSP_002934. Missing (in isoform IC158).
FT VARSPLIC 712 736 /FTid=VSP_002935. Missing (in isoform KI14 and isoform TRK).
FT VARSPLIC 737 750 /FTid=VSP_002936. Missing (in isoform KI25 and isoform TRK).
FT SEQUENCE 864 AA; 97063 MW; A202E93E208F636 CRC64;

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Query Match 51.3%; Score 2266.5; DB 1; Length 864;
Best Local Similarity 52.6%; Pred. No. 1,1e-124;
Matches 468; Conservative 107; Mismatches 206; Indels 109; Gaps 17;

Qy 10 PAMARLW-----GFCWL-VYGFWRARACPTCKSCSARIMCSPSPSGIAVAPPLP--- 60
Db 7 PACSEFWRITLDSVWLDVYG---SVLACPANCVCSTETINCRPPDGNL-FPLLEGDS 62

Qy 61 -----NSVD-PENITETIFIANQKRLIINEDDEAVYGLRLNLTIVDGLKFAVHA 110
Db 63 GNSNGASNIITDISKRITSIHLENMGLTILANVAMELYTGLOKLTIRKSGLRNIQPR 122

Qy 111 FLKNSNLQHINFRNKLTLSRKGFRLDISELLVGNPFTGSCDIMIKTLQE-AKSSP 169
Db 123 FAKNPRLRYINLSNRLLTTLTSMQLFQTLRSRELRBQNFNCSCDIMQMLQEGEARL 182

Qy 170 DTQDLYTLNASSKNIPLANIQINCGLPANLAAPNLTVEEGSITLSCVAGPVRMY 229
Db 183 DSQSLYCISADGSQLPFRNNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSLPDVD 242

Qy 230 MDVGNLVS-----KHMNETSHQSLRITNVISSDPSGKOISCVANLVGEODSDVNTLV 284
Db 243 WITGLOSINTHQTNLMTVVAINLTLVNTSEDNFTLTCLANVNGVMSASVALTV 302

Qy 285 PAPTTFLESPTSDHMCIPFTYKGNPKPALQWFPYNGALINESKYICTKJHVTNTEYH- 343
Db 303 YPRPVSVLVEPEVRLIEHCEIEFVVRGNPTPLTLMLYNGQPLRESKII-----HMDYYQ 354

Qy 344 -----GCLQLDNPTKANNEDYTLIANEYGEKQKQISAFPMGPGIDGANPYPDYIY 397
Db 355 EGEVSECCLEFNKPTHTNNGNYTLIANALGTINQTINGHFLKRP-----FPR--- 402

Qy 398 EDYGTANIDIGDTNRENEIPSTDVDTKGREHLSYAAVVAVIASVGFCL-LVLMFL-- 454
Db 403 -----STDFPDESASPTPTPTTTHKPEEDTFGSIANGLAFA--CVLLVLFMIN 454

Qy 455 KLAHRSKFGKGPASVISNDSDASPLMHTSNGSNTPSSBGGDAVIGTKTLPVIBNP 514
Db 455 KYGRBSKFGKGPAAVISGSDSASPLMHTINHGITTSLSLDAGDVTIVGTRIPVIBNP 514

Qy 515 QYFGITMSQLKPTPVQNHIGRHNIVLKRLEGEAGKFLAEVCYNLCPBODKILVAVKTL 574
Db 515 QYFQGNCHCKPPTYVOHKKRDYTLKRELGEAGKFLAEVCYNLSPTKDKMLVAAYAL 574

Qy 575 KDASDNARKDFHREBELTNLOHEHIVKRYGCVGEGDPLIMVEPYMGHGLNKLRLAHGP 634
Db 575 KDPTLARKDFOREBELTNLOHEHIVKRYGCVGEGDPLIMVEPYMGHGLNKLRLAHGP 634

Qy 635 DAVLMAEGNP---PTBELTQSQMLHIAQOIAAGWYLLASQHFVHRDLATRNCLVGENLLVK 691
Db 635 DAMILVDGQROKAGELGSLQMLHIASQIASGWYLLASQHFVHRDLATRNCLVGANLLVK 694

Qy 692 IGFQMSRDVYSTDYR-----VGGH 712
Db 695 IGFQMSRDVYSTDYREBPYQKGFSEVSWQOORLAASAATLFPNPGDNDFCIWCEVGH 754

Qy 713 TMLPIRMPBESIMYRFTTESDVMISGLVLMELFTYGGKQPVQOLSNNEVTECTOORVL 772
Db 755 TMLPIRMPBESIMYRFTTESDVMISGLVLMELFTYGGKQPVQOLSNNEVTECTOORVL 814

Qy 773 QRPRTCPQEVYELMLGCMQREPHRKNIKIHITLQMLAASPYVLDILG 822
Db 815 ERRRVCKEYVDVMLGCMQREPOORLNKIKIYKILHLAGATPIYLDILG 864

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Search completed: February 17, 2005, 00:27:28
Job time : 183 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 17, 2005, 00:18:38 ; Search time 45 Seconds
(without alignments)
1757,560 Million cell updates/sec

Title: US-10-645-546-2
4419
Perfect score: 1 MSSWIRWHPGPMARLMGFCW.....HTLLQNLAKASPYVLDILG 822
Sequence:

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR_79:.*
2: PIR1:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4419	100.0	822	1 A56853	brain-derived neur
2	4179.5	94.6	821	1 S06943	brain-derived neur
3	4162.5	94.2	821	1 A39667	brain-derived neur
4	3426	77.5	818	1 S44098	brain-derived neur
5	2520	57.0	477	1 I73631	brain-derived neur
6	2292.5	51.9	476	1 A35104	brain-derived neur
7	2289	51.8	825	2 A55178	neurotrophin-3 recep
8	2277	51.5	839	1 I73632	neurotrophin-3 recep
9	2275.5	51.5	474	1 C39667	brain-derived neur
10	2275.5	51.5	476	1 B39667	brain-derived neur
11	2252.5	51.0	852	2 I51259	tyrosine kinase C
12	2178	49.3	825	1 A40026	neurotrophin-3 recep
13	2149.5	48.6	803	1 S35695	neurotrophin-3 recep
14	1901	43.0	799	1 TVHUTB	nerve growth facto
15	1893.5	42.8	790	1 TVHUTB	nerve growth facto
16	1564	35.4	520	1 S44099	brain-derived neur
17	1420.5	32.1	282	2 I51236	brain-derived neur
18	1249	28.3	503	4 S23741	hypothetical TPR/T
19	989	22.4	612	2 I73633	gene trkC protein
20	856	19.4	871	2 I48696	protein-tyrosine k
21	856	19.4	881	1 I48697	protein-tyrosine k
22	850	19.2	525	1 A58674	neurotrophin-3 recep
23	798	18.1	945	1 A47299	neurotrophin-3 recep
24	749	16.9	685	1 A48289	neurotrophic recep
25	722	16.3	937	2 A45082	neurotrophic recep
26	703.5	15.9	943	2 B45082	neurotrophic recep
27	685.5	15.5	819	2 I48859	tyro 10 receptor k
28	679.5	15.4	1367	1 IGHUR1	insulin-like growth
29	676.5	15.3	1051	2 A39712	kinase-like protei

30	676	15.3	806	2 A35963	protein-tyrosine k
31	676	15.3	855	2 S42621	protein-tyrosine k
32	674	15.3	168	2 I51297	nerve growth facto
33	673.5	15.2	1371	2 A33837	insulin-like growth
34	672.5	15.2	800	2 A48991	heparin-binding gr
35	671.5	15.2	797	2 S38579	fibroblast growth
36	670.5	15.2	640	2 S23008	insulin-like growth
37	669.5	15.2	800	1 TVH02F	fibroblast growth
38	661	15.0	801	2 I55363	fibroblast growth
39	658	14.9	876	2 A49508	protein-tyrosine k
40	656	14.8	910	2 A53137	tyrosine kinase re
41	655	14.8	913	2 A48280	receptor tyrosine
42	654	14.8	806	1 TVH0D3	fibroblast growth
43	652.5	14.8	1070	2 JC4593	protein-tyrosine k
44	642	14.5	1363	2 T43220	insulin-like growth
45	640.5	14.5	819	1 TVCHFG	fibroblast growth

ALIGNMENTS

RESULT 1

A56853
Brain-derived neurotrophic factor receptor precursor - human
N:Alternate names: receptor tyrosine kinase trkB
C:Contains: protein-tyrosine kinase (EC 2.7.1.112)
C:Species: Homo sapiens (man)
C>Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
C:Accession: A56853; I56557
R:Nakagawara, A.; Lin, X.G.; Ikegaki, N.; White, P.S.; Yamashiro, D.J.; Nycum, L.M.; Bie
Genomic 25, 538-546, 1995
A:Title: Cloning and chromosomal localization of the human TRK-B tyrosine kinase recepto
A:Reference number: A56853; MIM:95309922; PMID:7789988
A:Accession: A56853
A:Molecule type: mRNA
A:Residues: 1-822 <NAK>
A:Cross-references: UNIPROT:Q16620; GB:U12140; NID:G525313; PIDN:AC53171.1; PID:G530791
R:Shilton, D.L.; Sutherland, J.; Gripp, J.; Camerato, T.; Armanini, M.P.; Phillips, H.S.
J. Neurosci. 15, 477-491, 1995
A:Title: Human trks: molecular cloning, tissue distribution, and expression of extracellular
A:Reference number: I56557; MIM:95123473; PMID:7823156
A:Accession: I56557
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-822 <SHR>
A:Cross-references: GB:S76473; NID:G913717; PIDN:AAB33109.1; PID:G913718
C:Genetics:
A:Gene: GDB:NTRK2; trkB
A:Cross-references: GDB:127898; OMIM:600456
A:Map position: 9q22.1-9q22.1
C:Function:
A:Description: regulation of nervous system development; receptor for brain-derived neur
C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycop
C:Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth factor
A:Map position: 9q22.1-9q22.1
F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-822/Product: brain-derived neurotrophic factor receptor #status predicted <MAT>
F:32-433/Domain: extracellular #status predicted <EXT>
F:67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:92-118/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:116-118/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LRR
F:436-452/Domain: transmembrane #status predicted <TM>
F:453-822/Domain: cytosolic #status predicted <CYT>
F:536-814/Domain: protein kinase homology <KIN>
F:544-552/Region: protein kinase ATP-binding motif
F:67-95, 121, 178, 205, 241, 254, 280, 325, 338, 350, 412/Binding site: carbohydrate (Aan) (covalen
F:572/Active site: lys #status predicted
F:706/Binding site: phosphate (Tyr) (covalent) #status predicted
F:817/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 100.0%; Score 4419; DB 1; Length 822;
Best Local Similarity 100.0%; Pred. No. 9e-204;

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Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSSWIRHGMAMRLMGFCMLVGFWRAPAFACPTSCCKSASRIWCDSPSGIVAFPLLEP 60
Db 1 MSSWIRHGMAMRLMGFCMLVGFWRAPAFACPTSCCKSASRIWCDSPSGIVAFPLLEP 60
QY 61 NSVDPENITFIANOKRLIINEDDVEAYVGLRNLTIVDSGLKFAVAKAFKNSNLOHI 120
Db 61 NSVDPENITFIANOKRLIINEDDVEAYVGLRNLTIVDSGLKFAVAKAFKNSNLOHI 120
QY 121 NFRNKLTSLSRKHFRHLDSLELLVGNPFTSCDIIWIKTLQBAKSSPTDOLYCLNES 180
Db 121 NFRNKLTSLSRKHFRHLDSLELLVGNPFTSCDIIWIKTLQBAKSSPTDOLYCLNES 180
QY 181 SKNPLANLOIPNCGSPSANLAAPNLTVBERGKSTITLSCSAGDPVPMYMDVGNLVSKM 240
Db 181 SKNPLANLOIPNCGSPSANLAAPNLTVBERGKSTITLSCSAGDPVPMYMDVGNLVSKM 240
QY 241 NETSHTQSLRITNISDDSGKOISCAVENLVGEDDQSVNLTVHAPATITFLSPSDH 300
Db 241 NETSHTQSLRITNISDDSGKOISCAVENLVGEDDQSVNLTVHAPATITFLSPSDH 300
QY 301 WCIPFTYKGNPKPALQMFYNGAILNESKYICTKIHTNHTHYGCLQLDNPTMANNQDYT 360
Db 301 WCIPFTYKGNPKPALQMFYNGAILNESKYICTKIHTNHTHYGCLQLDNPTMANNQDYT 360
QY 361 LIANKEYGDEKQISAHFMWPGIDGAPNYPDIYEDVGTANDIGDTTNSNEIPST 420
Db 361 LIANKEYGDEKQISAHFMWPGIDGAPNYPDIYEDVGTANDIGDTTNSNEIPST 420
QY 421 DVYDKTGRHLSTYAAVVVIVASVGFCLVMLFLKLARHSKFGMKGPASVISNDDBASP 480
Db 421 DVYDKTGRHLSTYAAVVVIVASVGFCLVMLFLKLARHSKFGMKGPASVISNDDBASP 480
QY 481 LHHISGNSPTSSSEGGPDVAVIIGMTKIPVIENPOYFGITNSQKPTFVOHIKRHNIYL 540
Db 481 LHHISGNSPTSSSEGGPDVAVIIGMTKIPVIENPOYFGITNSQKPTFVOHIKRHNIYL 540
QY 541 KRELGEAGFGKVFALACYNLCPEODKILVAVKTLKQASDNARKDPRHEABLLTNLOHEHI 600
Db 541 KRELGEAGFGKVFALACYNLCPEODKILVAVKTLKQASDNARKDPRHEABLLTNLOHEHI 600
QY 601 VKPFGVCVEBDPLIMVEFYMGKGLNKFLRAHGDVAVLMAEGNPTELTOGOMLHIAQOI 660
Db 601 VKPFGVCVEBDPLIMVEFYMGKGLNKFLRAHGDVAVLMAEGNPTELTOGOMLHIAQOI 660
QY 661 AAGWVYLASQHFVRDLATRNCLVGENLVKIGDPRGSRDYSIDYTRVGGHTMLPIRMM 720
Db 661 AAGWVYLASQHFVRDLATRNCLVGENLVKIGDPRGSRDYSIDYTRVGGHTMLPIRMM 720
QY 721 PPSISIMRKFTTSSDVSLSGLVLMWEIFTYGKQPMYQOLSNEVEICITQGRVLQRPCTPQ 780
Db 721 PPSISIMRKFTTSSDVSLSGLVLMWEIFTYGKQPMYQOLSNEVEICITQGRVLQRPCTPQ 780
QY 781 EYVELMLGCWQREPHMKNIKGIHTLLONLAKASPVYLDIIG 822
Db 781 EYVELMLGCWQREPHMKNIKGIHTLLONLAKASPVYLDIIG 822

RESULT 2
506943
brain-derived neurotrophic factor receptor precursor - mouse
N:Alternate names: receptor tyrosine kinase trkB
N:Contains: protein-tyrosine kinase (EC 2.7.1.112)
C:Species: Mus musculus (house mouse)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C:Accession: S06943
R:Klein, R.; Parada, L.F.; Coulier, F.; Barbacid, M.
EMBO J. 8, 3701-3709, 1989
A:Title: trkB, a novel tyrosine protein kinase receptor expressed during mouse neural de
A:Reference number: S06943; MUID:90059970; PMID:2555172
A:Accession: S06943
A:Molecule type: mRNA
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A:Residues: 1-821 <trkB>
A:Cross-references: UNIPROT:P15209; EMBL:X17647; NID:955505; PIDN:CAA5636.1; PID:955506
C:Genetics:
A:Gene: trkB
C:Function:
A:Description: regulation of nervous system development; receptor for brain-derived neurotrophic factor
C:Superfamily: nerve growth factor receptor; high affinity; leucine-rich alpha-2-glycoprotein
C:Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth factor 1
Inase
F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-821/Product: brain-derived neurotrophic factor receptor #status predicted <MAT>
F:32-434/Domain: extracellular #status predicted <EXT>
F:67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>
F:92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
F:116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
F:139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
F:435-451/Domain: transmembrane #status predicted <TM>
F:452-821/Domain: cytosolic #status predicted <CYT>
F:535-813/Domain: protein kinase homology <KIN>
F:543-551/Region: protein kinase ATP-binding motif
F:67,95,121,178,205,241,254,280,325,338,350,411/Binding site: carbohydrate (asn) (covalent)
F:571/Active site: lys #status predicted
F:706/Binding site: phosphate (Tyr) (covalent) #status predicted
F:816/Binding site: phosphate (Tyr) (covalent) #status predicted
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Query Match 94.6%; Score 4179.5; DB 1; Length 821;

Best Local Similarity 93.9%; Pred. No. 2,4e-192;

Matches 772; Conservative 27; Mismatches 22; Indels 1; Gaps 1;

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QY 1 MSSWIRHGMAMRLMGFCMLVGFWRAPAFACPTSCCKSASRIWCDSPSGIVAFPLLEP 60
Db 1 MSSWIRHGMAMRLMGFCMLVGFWRAPAFACPTSCCKSASRIWCDSPSGIVAFPLLEP 60
QY 61 NSVDPENITFIANOKRLIINEDDVEAYVGLRNLTIVDSGLKFAVAKAFKNSNLOHI 120
Db 61 NSVDPENITFIANOKRLIINEDDVEAYVGLRNLTIVDSGLKFAVAKAFKNSNLOHI 120
QY 121 NFRNKLTSLSRKHFRHLDSLELLVGNPFTSCDIIWIKTLQBAKSSPTDOLYCLNES 180
Db 121 NFRNKLTSLSRKHFRHLDSLELLVGNPFTSCDIIWIKTLQBAKSSPTDOLYCLNES 180
QY 181 SKNPLANLOIPNCGSPSANLAAPNLTVBERGKSTITLSCSAGDPVPMYMDVGNLVSKM 240
Db 181 SKNPLANLOIPNCGSPSANLAAPNLTVBERGKSTITLSCSAGDPVPMYMDVGNLVSKM 240
QY 241 NETSHTQSLRITNISDDSGKOISCAVENLVGEDDQSVNLTVHAPATITFLSPSDH 300
Db 241 NETSHTQSLRITNISDDSGKOISCAVENLVGEDDQSVNLTVHAPATITFLSPSDH 300
QY 301 WCIPFTYKGNPKPALQMFYNGAILNESKYICTKIHTNHTHYGCLQLDNPTMANNQDYT 360
Db 301 WCIPFTYKGNPKPALQMFYNGAILNESKYICTKIHTNHTHYGCLQLDNPTMANNQDYT 360
QY 361 LIANKEYGDEKQISAHFMWPGIDGAPNYPDIYEDVGTANDIGDTTNSNEIPST 420
Db 361 LIANKEYGDEKQISAHFMWPGIDGAPNYPDIYEDVGTANDIGDTTNSNEIPST 420
QY 421 DVYDKTGRHLSTYAAVVVIVASVGFCLVMLFLKLARHSKFGMKGPASVISNDDBASP 480
Db 421 DVYDKTGRHLSTYAAVVVIVASVGFCLVMLFLKLARHSKFGMKGPASVISNDDBASP 480
QY 481 LHHISGNSPTSSSEGGPDVAVIIGMTKIPVIENPOYFGITNSQKPTFVOHIKRHNIYL 540
Db 481 LHHISGNSPTSSSEGGPDVAVIIGMTKIPVIENPOYFGITNSQKPTFVOHIKRHNIYL 540
QY 541 KRELGEAGFGKVFALACYNLCPEODKILVAVKTLKQASDNARKDPRHEABLLTNLOHEHI 600
Db 541 KRELGEAGFGKVFALACYNLCPEODKILVAVKTLKQASDNARKDPRHEABLLTNLOHEHI 600
QY 601 VKPFGVCVEBDPLIMVEFYMGKGLNKFLRAHGDVAVLMAEGNPTELTOGOMLHIAQOI 660
Db 601 VKPFGVCVEBDPLIMVEFYMGKGLNKFLRAHGDVAVLMAEGNPTELTOGOMLHIAQOI 660
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Qy 661 AAGWVYLASQHFVHRDLATNCLVGENLVLKIGDFGMSRDVYSTDYRVGCHTMLPIRMM 720
 Db 660 AAGWVYLASQHFVHRDLATNCLVGENLVLKIGDFGMSRDVYSTDYRVGCHTMLPIRMM 719
 Qy 721 PPESIMVRKFTTSDVMSLGVLMELFTYKQKPWYQLSNNEVEICTIQGRVLOPRPCQ 780
 Db 720 PPESIMVRKFTTSDVMSLGVLMELFTYKQKPWYQLSNNEVEICTIQGRVLOPRPCQ 779
 Qy 781 EYVELMIGCQWRBPHRKNIKIGHTLLQNLAKASPVYLDILG 822
 Db 780 EYVELMIGCQWRBPHRKNIKIGHTLLQNLAKASPVYLDILG 821

RESULT 3

A39667
 brain-derived neurotrophic factor receptor precursor - rat
 N:Alternate names: receptor tyrosine kinase trkB.FL
 N:Contains: protein-tyrosine kinase (EC 2.7.1.112)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 09-Jul-2004
 C:Accession: A39667
 R:Middleman, D.S.; Lindberg, R.A.; Hunter, T.
 Mol. Cell. Biol. 11, 143-153, 1991
 A:Title: trkB, a neural receptor protein-tyrosine kinase: evidence for a full-length and
 A:Reference number: A39667; MUID:91094826; PMID:1846020
 A:Accession: A39667
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-821 <MID>
 A:Cross-references: UNIPROT:Q63604; GB:M55291; NID:9207473; PID:AAA42279.1; PID:9207474
 C:Function:
 A:Description: regulation of nervous system development; receptor for brain-derived neurotrophic factor
 C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycoprotein
 C:Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth factor kinase
 F:1-31/Domain: signal sequence #status predicted <SIG>
 F:32-821/Product: brain-derived neurotrophic factor receptor #status predicted <MAT>
 F:32-434/Domain: extracellular #status predicted <EXT>
 F:67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>
 F:92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
 F:116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
 F:139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
 F:435-451/Domain: transmembrane #status predicted <TM>
 F:452-821/Domain: cytosolic #status predicted <CYT>
 F:553-813/Domain: protein kinase homology <KIN>
 F:553-551/Region: protein kinase ATP-binding motif
 F:67,95,121,178,205,241,254,280,325,338,350,411/Binding site: carbohydrate (Aan) (covalent)
 F:571/Active site: lys #status predicted
 F:705/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
 F:816/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 94.2%; Score 4162.5; DB 1; Length 821;
 Best Local Similarity 93.6%; Pred. No. 1.6e-191;
 Matches 769; Conservative 25; Mismatches 27; Indels 1; Gaps 1;

Qy 1 MSSVIRHMGPMARLVGFCWLVGFWPAAFPSCSCSASRIWCPSPGIVAFPRLEP 60
 Db 1 MSPPRHMGPMARLVGFCWLVGFWPAAFPSCSCSASRIWCPSPGIVAFPRLEP 60
 Qy 61 NSVDPENITEIFIANOKRLIINDDVEAYVGLNLTIVDSGLKFAVAKFLKSNLQHI 120
 Db 61 NSIDPENITEIFIANOKRLIINDDVEAYVGLNLTIVDSGLKFAVAKFLKSNLQHI 120
 Qy 121 NFTNRKLTSLSRKPRHLDSELLVGNPFCSCDIMKIKLQKASPPQDLYCLANES 180
 Db 121 NFTNRKLTSLSRKPRHLDSELLVGNPFCSCDIMKIKLQKASPPQDLYCLANES 180
 Qy 181 SKNTPLANLOIPNCGLPBAPRLAARLVYBEGKSTISSVSGDPLFTLYMVGVNLSKRM 240
 Db 181 SKNTPLANLOIPNCGLPBAPRLAARLVYBEGKSTISSVSGDPLFTLYMVGVNLSKRM 240
 Qy 241 NETSHTOGLRITNISDDSGKOISCVANLVGSDQSVNLTVHFAPTITFLSPSPDH 300
 Db 241 NETSHTOGLRITNISDDSGKOISCVANLVGSDQSVNLTVHFAPTITFLSPSPDH 300

Db 241 NETSHTOGLRITNISDDSGKOISCVANLVGSDQSVNLTVHFAPTITFLSPSPDH 300
 Qy 301 WCIPTFVKNPKPALQWFGNALINBSKYICTKHVTNHTYHGCLOLDNPTMANNQDYT 360
 Db 301 WCIPTFVKNPKPALQWFGNALINBSKYICTKHVTNHTYHGCLOLDNPTMANNQDYT 360
 Qy 361 LIANREYKDEKOISAHFMWPGIDGANDPVYEDYGYAANDIGDTTNSNEIPST 420
 Db 361 LMANREYKDEKOISAHFMWPGIDGANDPVYEDYGYAANDIGDTTNSNEIPST 419
 Qy 421 DVMKRGREHLSYAAVAVVLSVVGFCLLVNLPLLLKARHSPKGPASVYSNDDASAP 480
 Db 420 DVADQTNREHLSYAAVAVVLSVVGFCLLVNLPLLLKARHSPKGPASVYSNDDASAP 479
 Qy 481 LHHISNGSNTPSSSEGGPDVITIGMTKIPITENPOYFGITNSOLKPTFOHIKRHHVYL 540
 Db 480 LHHISNGSNTPSSSEGGPDVITIGMTKIPITENPOYFGITNSOLKPTFOHIKRHHVYL 539
 Qy 541 KRELGEAGFGKVFLEACYNLCPEODKILVAVKTLKQASDNARQDFREAEILLNLQHEHI 600
 Db 540 KRELGEAGFGKVFLEACYNLCPEODKILVAVKTLKQASDNARQDFREAEILLNLQHEHI 599
 Qy 601 VKRTGVCVEGDDPLIMFEYKMGDLNFKLAHGPDAVLAEGNPPTLSTOSQMLHIAQOI 660
 Db 600 VKRTGVCVEGDDPLIMFEYKMGDLNFKLAHGPDAVLAEGNPPTLSTOSQMLHIAQOI 659
 Qy 661 AAGWVYLASQHFVHRDLATNCLVGENLVLKIGDFGMSRDVYSTDYRVGCHTMLPIRMM 720
 Db 660 AAGWVYLASQHFVHRDLATNCLVGENLVLKIGDFGMSRDVYSTDYRVGCHTMLPIRMM 719
 Qy 721 PPESIMVRKFTTSDVMSLGVLMELFTYKQKPWYQLSNNEVEICTIQGRVLOPRPCQ 780
 Db 720 PPESIMVRKFTTSDVMSLGVLMELFTYKQKPWYQLSNNEVEICTIQGRVLOPRPCQ 779
 Qy 781 EYVELMIGCQWRBPHRKNIKIGHTLLQNLAKASPVYLDILG 822
 Db 780 EYVELMIGCQWRBPHRKNIKIGHTLLQNLAKASPVYLDILG 821

RESULT 4

brain-derived neurotrophic factor receptor precursor - chicken
 N:Alternate names: receptor tyrosine kinase trkB
 N:Contains: protein-tyrosine kinase (EC 2.7.1.112)
 C:Species: Gallus gallus (chicken)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C:Accession: S59399; S42175; S44098
 R:Vin, N.O.; Erdmann, K.S.; Heumann, R.
 Gene 149, 383-384, 1994
 A:Title: Cloning and sequence analysis of a cDNA encoding a novel truncated form of the
 A:Reference number: S59398; MUID:95047511; PMID:7959025
 A:Accession: S59399
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-818 <VI2>
 A:Cross-references: UNIPROT:Q91987; EMBL:X77251; NID:9563881; PID:CAA54468.1; PID:94729
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1994
 R:Dechant, G.; Biffo, S.; Okazawa, H.; Kolbeck, R.; Potgiesser, J.; Berde, Y.A.
 Development 119, 545-558, 1993
 A:Title: Expression and binding characteristics of the BDNF receptor chick trkB.
 A:Reference number: S42175; MUID:94116452; PMID:8287802
 A:Accession: S42175
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-818 <DEC>
 A:Cross-references: EMBL:X74109; NID:9407798; PID:CAA52210.1; PID:9407799
 C:Genetics:
 A:Gene: trkB
 C:Function:
 A:Description: regulation of nervous system development; receptor for brain-derived neurotrophic factor
 C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycoprotein
 C:Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth factor kinase


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Db 181 SKNIPLANLOIPNCGLPANLAAPNLTVBEGKSTITLSCSYAGDPVPMYDVGNLYSKM 240
Qy 241 NETSHTOGSLRITNISDDSGKOISCAVENLVGEDODSVNLTVHFAPTITFLESPTSDDH 300
Db 241 NETSHTOGSLRITNISDDSGKOISCAVENLVGEDODSVNLTVHFAPTITFLESPTSDDH 300
Qy 301 WCIPFTVGNPKPALOMFYNGAILNESKYICTKIHTVNTHEHGCLQDNPPTMNNGDYT 360
Db 301 WCIPFTVGNPKPALOMFYNGAILNESKYICTKIHTVNTHEHGCLQDNPPTMNNGDYT 360
Qy 361 LIANKYGDKEKOISAHFMGPGIDDGANPNYPDVIYEDYGTAANDIGDTTNSNEIPST 420
Db 361 LIANKYGDKEKOISAHFMGPGIDDGANPNYPDVIYEDYGTAANDIGDTTNSNEIPST 420
Qy 421 DVTDKTGRHLSYAAVVAVIASVVGFCILVWLFLKLARSHKFGMKG 466
Db 421 DVTDKTGRHLSYAAVVAVIASVVGFCILVWLFLKLARSHKFGMKG 466
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RESULT 6

```
A35104
brain-derived neurotrophic factor receptor precursor, short splice form - mouse
N/Alternate names: truncated receptor tyrosine kinase trkB
C/Species: Mus musculus (house mouse)
C/Date: 07-Sep-1990 #sequence_revision 06-Nov-1992 #text_change 11-Jun-1999
C/Accession: A35104
R/Klein, R.; Conway, D.; Parada, L.F.; Barbacid, M.
Cell 61, 647-656, 1990
A/Title: The trkB tyrosine protein kinase gene codes for a second neurogenic receptor th
A/Reference number: A35104; MUID:90263089; PMID:2160854
A/Accession: A35104
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-476 <KLB>
A/Cross-references: GB:33385; NID:g202158; PIDN:AAA40482.1; PID:g202159
C/Comment: This form of the receptor is missing the protein kinase domain.
C/Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycopr
C/Keywords: alternative splicing; glycoprotein; growth factor receptor; tandem repeat; t
F/1-31/Domain: signal sequence #status predicted <SIG>
F/32-476/Product: brain-derived neurotrophic factor receptor, short splice form #status
F/32-434/Domain: extracellular #status predicted <EXT>
F/67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F/92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F/116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F/139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR
F/435-451/Domain: cytosolic #status predicted <CYT>
F/452-476/Domain: transmembrane #status predicted <TM>
F/67,95,121,178,205,241,254,280,325,338,350,411/Binding site: carbohydrate (Aan) (coval
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Query Match 51.8%; Score 2292.5; DB 1; Length 476;
Best Local Similarity 89.7%; Pred. No. 1.5e-102;
Matches 418; Conservative 27; Mismatches 20; Indels 1; Gaps 1;

Qy 1 MSWIRHMGPMALMGFCMLVGFWRAPACPTSCCKSASRIWCSDPSPGIVAFPLRP 60
Db 1 MSPPLKMHGPMALMGICLVGFWRASLACPTSCCKSASRIWCTSPGIVAFPLRP 60
Qy 61 NSVDPENITEIFIANOKRELIINEDVEAYVGLNLTIVDSGLKFAVHAFAFKNSNTQHI 120
Db 61 NSVDPENITEIFIANOKRELIINEDVEAYVGLNLTIVDSGLKFAVHAFAFKNSNTQHI 120
Qy 121 NPTNKTLSLRKAFRHLDSELLVGNPFTCSCDIMWIKTLQAKSSPDYDLYCINES 180
Db 121 NPTNKTLSLRKAFRHLDSELLVGNPFTCSCDIMWIKTLQAKSSPDYDLYCINES 180
Qy 181 SKNIPLANLOIPNCGLPANLAAPNLTVBEGKSTITLSCSYAGDPVPMYDVGNLYSKM 240
Db 181 SKNIPLANLOIPNCGLPANLAAPNLTVBEGKSTITLSCSYAGDPVPMYDVGNLYSKM 240
Qy 241 NETSHTOGSLRITNISDDSGKOISCAVENLVGEDODSVNLTVHFAPTITFLESPTSDDH 300
Db 241 NETSHTOGSLRITNISDDSGKOISCAVENLVGEDODSVNLTVHFAPTITFLESPTSDDH 300
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Qy 301 WCIPFTVGNPKPALOMFYNGAILNESKYICTKIHTVNTHEHGCLQDNPPTMNNGDYT 360
Db 301 WCIPFTVGNPKPALOMFYNGAILNESKYICTKIHTVNTHEHGCLQDNPPTMNNGDYT 360
Qy 361 LIANKYGDKEKOISAHFMGPGIDDGANPNYPDVIYEDYGTAANDIGDTTNSNEIPST 420
Db 361 LIANKYGDKEKOISAHFMGPGIDDGANPNYPDVIYEDYGTAANDIGDTTNSNEIPST 420
Qy 421 DVTDKTGRHLSYAAVVAVIASVVGFCILVWLFLKLARSHKFGMKG 466
Db 421 DVTDKTGRHLSYAAVVAVIASVVGFCILVWLFLKLARSHKFGMKG 466
```

RESULT 7

```
A55178
neurotrophin receptor trkC precursor - human
C/Species: Homo sapiens (man)
C/Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 18-Jun-1999
C/Accession: A55178
R/McGregor, L.M.; Baylín, S.B.; Griffin, C.A.; Hawkins, A.L.; Nelkin, B.D.
Genomics 22, 267-272, 1994
A/Title: Molecular cloning of the cDNA for human TrkC (NTRK3), chromosomal assignment, a
A/Reference number: A55178; MUID:95104834; PMID:7806211
A/Accession: A55178
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-825 <MG>
A/Cross-references: GB:U05012; NID:g442389; PIDN:AA75374.1; PID:g442390
C/Genes: NTRK3
A/Map position: 15q24-15q25
C/Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycopr
C/Keywords: alternative splicing; ATP; growth factor receptor
F/79-103/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F/104-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F/128-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F/151-162/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR
F/536-817/Domain: protein kinase homology <KIN>
F/544-552/Region: protein kinase ATP-binding motif
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Query Match 51.8%; Score 2289; DB 2; Length 825;
Best Local Similarity 54.4%; Pred. No. 4e-102;
Matches 466; Conservative 111; Mismatches 199; Indels 80; Gaps 17;

Qy 10 PMAARLM-----GFCWL-VGFWRAAPACTSCCKSASRIWCSDPSPGIVAFPLRP--- 60
Db 7 PACCSFMRIRFLQSVMLDVG---SVLACPANCVCSTETINCRPPDGNL-FPLLEGQDS 62
Qy 61 -----NSVD-PENITEIFIANOKRELIINEDVEAYVGLNLTIVDSGLKFAVHA 110
Db 63 GNSNGNANINITITISRNITSIHLENWRSLLTIANVDMLTYGLOKLTIKNSGLRSIPRA 122
Qy 111 FLKNSNLOHINPTNKTLSLRKAFRHLDSELLVGNPFTCSCDIMWIKTLQOE-AKSSP 169
Db 123 FANPNHRIYINLSNRNLTITLSWQLFQTLSLRELQLEGNFPNCGSDIMWLMQEGSAKL 182
Qy 170 DTQDLYCINESKNIPLANLOIPNCGLPANLAAPNLTVBEGKSTITLSCSYAGDPVPMY 229
Db 183 NSOILYCINADGSQLPLFRNNISQCDLBEISVSHVNLTVBEGNAVITTCNGSGPLDVD 242
Qy 230 WDVGNLYS-----KNNHSTHOGSLRITNISDDSGKOISCAVENLVGEDODSVNLTVH 284
Db 243 WITVGLQSLNTHOQNTLWVAHINLTLVAVTSDSKFTLTJLAENVVAGSNASVALTVY 302
Qy 302 WITVGLQSLNTHOQNTLWVAHINLTLVAVTSDSKFTLTJLAENVVAGSNASVALTVY 302
Db 303 YPRVYVLSLEPRRLRHCIFVVRGNRPPTLHNLHNGQPLRESKLI-----HVEYIQ 354
Qy 344 -----GCLQDNPPTMNNGDYTLLANKYGDKEKOISAHFMGPGIDDGANPNYPD--- 394
Db 355 EGEISBQCLFNRPPTHYNNGNVYLLIANPLGTANQTINGHFLKEP-----PPESTD 405
```

Qy 395 --VIEDYGTAAANDIGDITNRSNEIPSTDTYDKTGRHLSVYAVVYASVGC-LLVWL 451
Db 406 NFILEDV-----SPTPIYTHKREBDTFCVJAVGLAARA--CVLLVVL 449
Qy 452 FLI--KLARHSKFGMKGPASVISNDSDASPLHHISNGSNTSPSSGEGPDAVIIGMTKIP 509
Db 450 FVMINKYGRSKFGMKGPVAVISGEEDSAPLHHINNGITTPSSLDAGPDTVIIGMTKIP 509
Qy 510 VIENPOYFGITNSQLKPDYVQHIKRNIYVKRELGGAFKQVFLACVNLCPEDOKILV 569
Db 510 VIEHPQYFQGHNGHCKPDYVQHIKRDIYVKRELGGAFKQVFLACVNLSPKDKMLV 569
Qy 570 AVKTLKASDARAKDFRBAELTNLQHEHIVKRYGVCGVGDPLIMFEVYMKGDINKFL 629
Db 570 AVKALKDPITLAAKDFRBAELTNLQHEHIVKRYGVCGVGDPLIMFEVYMKGDINKFL 629
Qy 630 RAHGPDAVLABGNP---PTELTSQOMLHIAQOIAAGVYVLASQHFVHRDLATRNCLVGE 686
Db 630 RAHGPDAVLABGNP---PTELTSQOMLHIAQOIAAGVYVLASQHFVHRDLATRNCLVGA 689
Qy 687 NLVKTIDFGMSRDVYSTDYRYVCGHTMLPIRMPPESIMYRKTTESDYVSLGVLMET 746
Db 690 NLVKTIDFGMSRDVYSTDYRYVCGHTMLPIRMPPESIMYRKTTESDYVSLGVLMET 749
Qy 747 FTYGKOPMYOLSNNEVEICTQGRVLOPRPTCPQEVYELMGCMQREPHMKXIKGITHL 806
Db 750 FTYGKOPMYOLSNNEVEICTQGRVLOPRPTCPQEVYELMGCMQREPHMKXIKGITHL 809
Qy 807 LQNLAKASPVYLDILG 822
Db 810 LHALGKATPIYLDILG 825

RESULT 8

173632
neurotrophin-3 receptor precursor - human
N:Alternate names: receptor tyrosine kinase trkC
C:Species: Homo sapiens (man)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C/Accession: I73632

R:Shelton, D.L.; Sutherland, J.; Grifp, J.; Camerato, T.; Armanini, M.P.; Phillips, H.S.
J. Neurosci. 15, 477-491, 1995
A:Title: Human trks: molecular cloning, tissue distribution, and expression of extracell
A:Reference number: 156557; MUID:95123473; PMID:7823156
A/Accession: I73632
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-839 <RES>
A:Cross-references: UNIPROT:Q16288; GB:S76475; NID:G913721; PIND:AA03111.1; PID:G913722
C/Genetic: A:Gene: GDB:NTRK3; TRKC
A:Cross-references: GDB:127899; OMIM:191316
A:Map position: 15q24-15q25
C:Function: A:Description: regulation of nervous system development; receptor for neurotrophin-3
C:Superfamily: nerve growth factor receptor; high affinity; leucine-rich alpha-2-glycop
C:Keywords: ATP; autophosphorylation; brain; glycoprotein; growth factor receptor; phosp
F:1-31/Domin: signal sequence #status predicted <SIG>
F:33-839/Product: neurotrophin-3 receptor #status predicted <MAT>
F:33-436/Domin: extracellular #status predicted <EXT>
F:79-103/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:104-127/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:128-150/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:151-162/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:437-453/Domin: transmembrane #status predicted <TMN>
F:454-839/Domin: cytosolic #status predicted <CYT>
F:536-831/Domin: protein kinase homology <KIN>
F:544-552/Region: protein kinase ATP-binding motif
F:72,79,133,153,203,218,232,259,267,294,375,386/Binding site: carbohydrate (Asn) (cc
F:572/active site: lys #status predicted
F:709/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
F:834/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 51.5%; Score 2277; DB 1; Length 839;
Best Local Similarity 53.7%; Pred. No. 1,5e-101;
Matches 467; Conservative 110; Mismatches 199; Indels 94; Gaps 18;

Qy 10 PAMARLW-----GFCWL-VVGFRAAFACPTSCKCSASRWCSDPSPGIVAPRLAR--- 60
Db 7 PAKCSFMRJFLDSWLDIVG---SVLACANVCSTKTEINCRPDDGNL-FLLBSQDS 62
Qy 61 -----NSVD-PENITEIFIANOKRLEINEDVBAVVGRLNITVDSGLKFAHKA 110
Db 63 GNSGNANINITDISNRTSIHLENWRSLSHTLAAVMELYTGLOKLTIKNSGLRSIQPRA 122
Qy 111 FLKNSLQINFRANKLTSLSRKHFRHDLSELIVGNPPTGCDIMTITLDE-AKSP 169
Db 123 FAKNPRLRYINLSNRLTTLISWQLFOTLSRLQLQNFNCSCDIRMWLMQEOGAKL 182
Qy 170 DTODLYCLNESSKNIPLANQIPNCGPSANLAPNLTVYEGSITLSGVAQDPVNNY 229
Db 183 NSQNLICINADSGQLPFRKNISQCDLPISVSHVNLTVARGDNNAVITTCGSGPLDVD 242
Qy 230 MDVGNLVS-----KHNETSHTQSLRTNITSDDSGKOISCYAENLVGEDSDVNLTVH 284
Db 243 MIVTGLQSIINTHOTNLMTVHAINTLVVTSBEDNGFTLTCLAEVNVGKSNASVALTVY 302
Qy 285 FAPTITFLESPTSDHMCIPFTYKGNPKPALQVFNCAIINSEKTYICTKHVNTTEYH- 343
Db 303 YPRVVSLEBEPLRLRHCIEFVVRGNPPTLHWLHNGQPRBSKII-----HVEYQ 354
Qy 344 -----GCLQDNPTHMNGDYTLIAKNEYGKQKOISAFHFMQPGIDGANDPNYPD--- 394
Db 355 EGEISRGCLFNPFTHYNNQNTYLAKNPLGTANQITINGHFLKP-----PFESTD 405
Qy 395 --VIEDYGTAAANDIGDITNRSNEIPSTDTYDKTGRHLSVYAVVYASVGC-LLVWL 451
Db 406 NFILEDV-----SPTPIYTHKREBDTFCVJAVGLAARA--CVLLVVL 449
Qy 452 FLI--KLARHSKFGMKGPASVISNDSDASPLHHISNGSNTSPSSGEGPDAVIIGMTKIP 509
Db 450 FVMINKYGRSKFGMKGPVAVISGEEDSAPLHHINNGITTPSSLDAGPDTVIIGMTKIP 509
Qy 510 VIENPOYFGITNSQLKPDYVQHIKRNIYVKRELGGAFKQVFLACVNLCPEDOKILV 569
Db 510 VIEHPQYFQGHNGHCKPDYVQHIKRDIYVKRELGGAFKQVFLACVNLSPKDKMLV 569
Qy 570 AVKTLKASDARAKDFRBAELTNLQHEHIVKRYGVCGVGDPLIMFEVYMKGDINKFL 629
Db 570 AVKALKDPITLAAKDFRBAELTNLQHEHIVKRYGVCGVGDPLIMFEVYMKGDINKFL 629
Qy 630 RAHGPDAVLABGNP---PTELTSQOMLHIAQOIAAGVYVLASQHFVHRDLATRNCLVGE 686
Db 630 RAHGPDAVLABGNP---PTELTSQOMLHIAQOIAAGVYVLASQHFVHRDLATRNCLVGA 689
Qy 687 NLVKTIDFGMSRDVYSTDYRYVCGHTMLPIRMPPESIMYRKTTESDYVSLGVLMET 746
Db 690 NLVKTIDFGMSRDVYSTDYRYVCGHTMLPIRMPPESIMYRKTTESDYVSLGVLMET 749
Qy 747 FTYGKOPMYOLSNNEVEICTQGRVLOPRPTCPQEVYELMGCMQREPHMKXIKGITHL 806
Db 750 FTYGKOPMYOLSNNEVEICTQGRVLOPRPTCPQEVYELMGCMQREPHMKXIKGITHL 809
Qy 807 LQNLAKASPVYLDILG 822
Db 810 EPOGRINIKIYILHALGKATPIYLDILG 839

RESULT 9

C39667
brain-derived neurotrophic factor receptor precursor, splice form T2 - rat
N:Alternate names: truncated receptor tyrosine kinase trkB.T2
C:Species: Rattus norvegicus (Norway rat)
C>Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 09-Jul-2004
C/Accession: C39667

R,Middlemas, D.S.; Lindberg, R.A.; Hunter, T.
 Mol. Cell. Biol. 11, 143-153, 1991
 A>Title: trkb, a neural receptor protein-tyrosine kinase: evidence for a full-length and
 A/Reference number: A39667; PMID:91094826; PMID:1846020
 A/Accession: C39667
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-474 <MDS>
 A/Cross-references: UNIPROT:Q63604; GB:M55293; NID:9207477; PIDN:AAA42280.1; PID:9207478
 C/Comment: This form of the receptor is missing the protein kinase domain.
 C/Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycopr
 C/Keywords: alternative splicing; glycoprotein; growth factor receptor; tandem repeat; t
 F/1-31/Domain: signal sequence #status predicted <SIG>
 F/32-474/Product: brain-derived neurotrophic factor receptor, splice form T2 #status pre
 F/32-474/Domain: extracellular #status predicted <EXT>
 F/67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
 F/92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F/116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 F/139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology #atypical <LR
 F/435-451/Domain: transmembrane #status predicted <TMN>
 F/452-474/Domain: cytosolic #status predicted <CYT>
 F/67,95,121,178,205,241,254,280,325,338,350,411/Binding site: carbohydrate (Aan) (coval

Query Match 51.5%; Score 2275.5; DB 1; Length 474;
 Best local similarity 89.1%; Pred. No. 9.5e-102;
 Matches 415; Conservative 25; Mismatches 25; Indels 1; Gaps 1;

Qy 1 MSSIRRHGPMALMGFCMLVGFWRAPACPTSCSKSARICSDPSRGIAPRLEP 60
 Db 1 MSPPRHGMAMLMGCLLVGFWRASLACPMSCSTTRICWCTEBSPEIAPRLEP 60
 Qy 61 NSVDPENITFIANOKRLIINDDVEAYVGLNLTIVDSGLKFAVHAKAFKXSNLOHI 120
 Db 61 NSIDPENITELIANOKRLIINDDVEAYVGLNLTIVDSGLKFAVHAKAFKXSNLOHI 120
 Qy 121 NFRNKLTSLSRKHFRLDSEILVGNPFTSCDIMWIKTLQBAKSSPTODLYCLNES 180
 Db 121 NFRNKLTSLSRRHFRHLDSDILITGNPFTSCDIMWIKTLQBAKSSPTODLYCLNES 180
 Qy 181 SKNPLANLOIPNCGLPBANLAAPNLVTEBKSITLSCSVAGDPVPMYVGNLVSKM 240
 Db 181 SKNPLANLOIPNCGLPBANLAAPNLVTEBKSITLSCSVAGDPVPMYVGNLVSKM 240
 Qy 241 NETSHTGSLRTINISSDDSGKQISCAVENLVGEDQSVNLTVHAPATTITLESPTSDDH 300
 Db 241 NETSHTGSLRTINISSDDSGKQISCAVENLVGEDQSVNLTVHAPATTITLESPTSDDH 300
 Qy 301 WCIPFTYKGNPKPALQWFGYNGAILNESKYICTKIHVNTHTYHGCLOLDNPTNNNGDYT 360
 Db 301 WCIPFTYKGNPKPALQWFGYNGAILNESKYICTKIHVNTHTYHGCLOLDNPTNNNGDYT 360
 Qy 361 LIANNEYGKDEKQISAFPMGPGIDGAPNYPVYIYEDYGTANDIGDTTNRSENPST 420
 Db 361 LIANNEYGKDEKQISAFPMGPGIDGAPNYPVYIYEDYGTANDIGDTTNRSENPST 420
 Qy 421 DVMDKTRGHEHLSYAVVAVVIVASVGFCLLVMLFLIKLARHSKFGMKG 466
 Db 421 DVMDKTRGHEHLSYAVVAVVIVASVGFCLLVMLFLIKLARHSKFGMKG 466

RESULT 10
 B39667
 brain-derived neurotrophic factor receptor precursor, splice form T1 - rat
 N/Alternate names: truncated receptor tyrosine kinase trkb.T1
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 09-Jul-2004
 C/Accession: B39667
 R/Middlemas, D.S.; Lindberg, R.A.; Hunter, T.
 Mol. Cell. Biol. 11, 143-153, 1991
 A>Title: trkb, a neural receptor protein-tyrosine kinase: evidence for a full-length and
 A/Reference number: A39667; PMID:91094826; PMID:1846020
 A/Accession: B39667
 A/Status: preliminary

A/Molecule type: mRNA
 A/Residues: 1-476 <MDS>
 A/Cross-references: UNIPROT:Q63604; GB:M55292; NID:9207475; PIDN:AAA42280.1; PID:9207476
 C/Comment: This form of the receptor is missing the protein kinase domain.
 C/Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycopr
 C/Keywords: alternative splicing; glycoprotein; growth factor receptor; tandem repeat; t
 F/1-31/Domain: signal sequence #status predicted <SIG>
 F/32-476/Product: brain-derived neurotrophic factor receptor, splice form T1 #status pre
 F/32-476/Domain: extracellular #status predicted <EXT>
 F/67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
 F/92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F/116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 F/139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology #atypical <LR
 F/435-451/Domain: transmembrane #status predicted <TMN>
 F/452-476/Domain: cytosolic #status predicted <CYT>
 F/67,95,121,178,205,241,254,280,325,338,350,411/Binding site: carbohydrate (Aan) (coval

Query Match 51.5%; Score 2275.5; DB 1; Length 476;
 Best local similarity 89.1%; Pred. No. 9.5e-102;
 Matches 415; Conservative 25; Mismatches 25; Indels 1; Gaps 1;

Qy 1 MSSIRRHGPMALMGFCMLVGFWRAPACPTSCSKSARICSDPSRGIAPRLEP 60
 Db 1 MSPPRHGMAMLMGCLLVGFWRASLACPMSCSTTRICWCTEBSPEIAPRLEP 60
 Qy 61 NSVDPENITFIANOKRLIINDDVEAYVGLNLTIVDSGLKFAVHAKAFKXSNLOHI 120
 Db 61 NSIDPENITELIANOKRLIINDDVEAYVGLNLTIVDSGLKFAVHAKAFKXSNLOHI 120
 Qy 121 NFRNKLTSLSRKHFRLDSEILVGNPFTSCDIMWIKTLQBAKSSPTODLYCLNES 180
 Db 121 NFRNKLTSLSRRHFRHLDSDILITGNPFTSCDIMWIKTLQBAKSSPTODLYCLNES 180
 Qy 181 SKNPLANLOIPNCGLPBANLAAPNLVTEBKSITLSCSVAGDPVPMYVGNLVSKM 240
 Db 181 SKNPLANLOIPNCGLPBANLAAPNLVTEBKSITLSCSVAGDPVPMYVGNLVSKM 240
 Qy 241 NETSHTGSLRTINISSDDSGKQISCAVENLVGEDQSVNLTVHAPATTITLESPTSDDH 300
 Db 241 NETSHTGSLRTINISSDDSGKQISCAVENLVGEDQSVNLTVHAPATTITLESPTSDDH 300
 Qy 301 WCIPFTYKGNPKPALQWFGYNGAILNESKYICTKIHVNTHTYHGCLOLDNPTNNNGDYT 360
 Db 301 WCIPFTYKGNPKPALQWFGYNGAILNESKYICTKIHVNTHTYHGCLOLDNPTNNNGDYT 360
 Qy 361 LIANNEYGKDEKQISAFPMGPGIDGAPNYPVYIYEDYGTANDIGDTTNRSENPST 420
 Db 361 LIANNEYGKDEKQISAFPMGPGIDGAPNYPVYIYEDYGTANDIGDTTNRSENPST 420
 Qy 421 DVMDKTRGHEHLSYAVVAVVIVASVGFCLLVMLFLIKLARHSKFGMKG 466
 Db 421 DVMDKTRGHEHLSYAVVAVVIVASVGFCLLVMLFLIKLARHSKFGMKG 466

RESULT 11
 I51259
 tyrosine kinase C receptor - chicken
 C/Species: Gallus gallus (chicken)
 C/Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
 C/Accession: I51259
 R/Gartner, A.S.; Large, T.H.
 Neuron 13, 457-472, 1994
 A>Title: Isoforms of the avian TrkC receptor: a novel kinase insertion dissociates trans
 A/Reference number: I51259; PMID:94338700; PMID:8060621
 A/Accession: I51259
 A/Status: preliminary; translated from GB/EMBL/DDBJ
 A/Molecule type: mRNA
 A/Residues: 1-852 <GAR>
 A/Cross-references: UNIPROT:Q91044; GB:S74248; NID:g712820; PIDN:AA831699.1; PID:g712821
 C/Genetics: trkb
 C/Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycopr
 F/79-103/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

F:538-844/Domain: protein kinase homology <KIN>

```

Query Match      51.0%; Score 2252.5; DB 2; Length 852;
Best Local Similarity 52.7%; Pred. No. 2,36-100;
Matches 463; Conservative 114; Mismatches 204; Indels 97; Gaps 18;

Qy 10 PAMARLWG--FCWLVVG-FWMAAFACPTSCCKSARIMCSDPSGIVAPRLBP----- 60
Db 7 PTKCTFRVLLWIMIGDYLLSVLACPAKCLCSKTDINCKKPPDDGN--FPLLSQDSGSS 65
Qy 61 -----NSVD--PENITEIFIANOKRLRIINEDVEAVVGLRLITVDSGLKFAVHAKFLK 113
Db 66 NGNTSINITDSIRNITSIHIENMNLOTLNAVDELTGLORLTIRSGLRNIOPRAFAK 125
Qy 114 NSNIQIHNFTNKLTSLSRKHFRHLDELIVGNPPTSCDDIMWITLQAE-AKSPDTQ 172
Db 126 NPHRLYIDLSGNRLTTLTSMQLFQTLRLFDLIRNPFSCDIDIMWILQMBEGKANLQSQ 185
Qy 173 DLYCLNSSKNIPLANQIPNCGIPSNALAPNLTVEBGSITLSCVAQDPVPMNTWV 232
Db 186 QLRHGMNLDYAVILRRNMNITQCDPEISVSHVNLTVBGENAVITTCNGSGPLPDVMTV 245
Qy 233 GNLVS-----KHNMTSHTQSLRITNISDDSGKQISCAENLVGEDODSVNLTVAFAF 287
Db 246 ADLHSINTHOTNLMTNVAHNLTLVNTSBDNGLFLTCLAENVGSMNSVLLTYVYFP 305
Qy 288 TITLESPTSDHMCIPFTVKGPNKPAQWFNGAALINESKYICTKIHVTNHTBYH--- 343
Db 306 RILLESPEVLHLEHCIAFAVHGNAPFLHMLHNGQVLRRETI-----HMEFYQGE 357
Qy 344 ---GCLQDLPNTNMGDYLTLAKNEYCKDEKQISAPFMGPGIDGDANPVYD-----V 395
Db 358 VSECLLFNKPRTNHNNGYITVAITNQLASANTQIKGHLEXP-----FPESTDNFV 408
Qy 396 IYEVGTAANDIGDTNRSNEIPSTDVTDKTRGHEHLSVAAVVIASVVGFC-LIYMLFLL 454
Db 409 SIGDY-----EVSPT-----PRTVTHKREBDTFCGSIANGLAFA--CYLLVVLFFIM 454
Qy 455 --KLARHSKFGMKGPASVISNDSDASPLHHISNGSNTSSSEGGPDAVIIGMTKIPVIE 512
Db 455 INKYGRRSKFGMKGPVAVISGEBDSASPLHHINHGITTPSSLDAGPDTVVGMRIPVIE 514
Qy 513 NPQYFGITNSQLKBDTPVOHKKRNIVYLRKELGAGRGKVLACNYLCPRODKILVAVK 572
Db 515 NPQYFGOHCHCKPDTVOHKKRDYVLRKELGAGAFKVLACNYLSPINDMLVAVK 574
Qy 573 TLKASDARAKFREAEFLTNLOHEHIVKFGYCVESGDPILIMFEYMKHGDMLKFLRAH 632
Db 575 ALKOPTLAARKDFOREAEFLTNLOHEHIVKFGYCGGDDPLIMFEYMKHGDMLKFLRAH 634
Qy 633 GPDAVLMAKGNP---PTBELTOSOMLHIAQOIAAGVVIASQHPVHRDLATBNCLVGEHLL 689
Db 635 GPDAMLIVDQGPQAKGELGSLQMLHIASQIASGVVVIASQHPVHRDLATBNCLVGNL 694
Qy 690 VKIDGFGMSRIVYSTDYR-----VGHTMLPIIMWBPES 724
Db 695 VKIDPFGMSRIVYSTDYRBPGRPKQLSTAMORHRLAPAAATVGGHTMLPIIMWBPES 754
Qy 725 IMYKFTTESDVMSLGVVLEIFTYGGKOPWYOLSNNEVIECTIGQVLYORRTPQOEYVE 784
Db 755 IMYKFTTESDVMSFGVILMEIFTYGGKOPWYOLSNNEVIECTIGQVLYORRTPQOEYVD 814
Qy 785 LMLGCMOREPFRMRKNIKGIHTLLONLAKASPVYLDILG 822
Db 815 LMLGCMOREPQORLNIKIYKILHMLKATPIYLDILG 852

```

RESULT 12
A40026
neurotrophin-3 receptor precursor - pig

N:Alternate names: receptor tyrosine kinase trkC
N:Contains: protein-tyrosine kinase (EC 2.7.1.112)
C:Species: Sus scrofa domestica (domestic pig)

C>Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 09-Jul-2004

C/Accession: A40026

R:Lamballe, F.; Klein, R.; Barbacid, M.

A/Cell: 66, 967-979, 1991

A/Title: trkC, a new member of the trk family of tyrosine protein kinases, is a receptor

A/Reference number: A40026; MUID:91364178; PMID:1653651

A/Accession: A40026

A/Molecule type: mRNA

A/Residues: 1-825 <LAM>

A/Cross-references: UNIPROT:P24786; GB:M80800; NID:g164698; PIDN:AAA31130.1; PID:g164699

A/Experimental source: adult brain

C/Function:

A>Description: regulation of nervous system development; receptor for neurotrophin-3

C/Superfamily: nerve growth factor receptor; high affinity; leucine-rich alpha-2-glycopr

C/Keywords: ATP; autophosphorylation; brain; glycoprotein; growth factor receptor; phospt

F:1-31/Domain: signal sequence #status predicted <SIG>

F:32-825/Product: neurotrophin-3 receptor #status predicted <MAT>

F:32-436/Domain: extracellular #status predicted <EXT>

F:79-103/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRP1>

F:104-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRP2>

F:128-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRP3>

F:151-162/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LRF

F:437-453/Domain: transmembrane #status predicted <CYT>

F:454-825/Domain: cytosolic #status predicted <CYT>

F:536-817/Domain: protein kinase homology <KIN>

F:544-552/Region: protein kinase ATP-binding motif

F:568,72,79,133,163,203,218,232,259,267,272,294,375,388/Binding site: carbohydrate (asn)

F:572/Active site: lys #status predicted

F:709/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

F:820/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 49.3%; Score 2178; DB 1; Length 825;

Best Local Similarity 52.9%; Pred. No. 7,86-97;

Matches 454; Conservative 105; Mismatches 214; Indels 86; Gaps 19;

```

Qy 10 PAMARLWG--FCWLVVG-FWMAAFACPTSCCKSARIMCSDPSGIVAPRLBP--- 60
Db 7 PAKCSFMRIFLDSVWLDYVG---SVLACPAKCVCSSTETINCRPPDDGN--FPLLSQDS 62
Qy 61 -----NSVD--PENITEIFIANOKRLRIINEDVEAVVGLRLITVDSGLKFAVHAKA 110
Db 63 GNSGNASINITDSIRNITSIHIENMRGHTLNAVDELTGLOKLTNKGSLRSIQRA 122
Qy 111 PLKNSNIQIHNFTNKLTSLSRKHFRHLDELIVGNPPTSCDDIMWITLQAE-AKSP 169
Db 123 FAKNPHRLYINLSSNRLTTLTSMQLFQTLRLREIRLEBGNPFNCSCDIRMWLOBOGAKL 182
Qy 170 DTQDLYCLNSSKNIPLANQIPNCGIPSNALAPNLTVEBGSITLSCVAQDPVPMNY 229
Db 183 NSQSLYCTISADGSQLPLFRNNISQCDPEISVSHVNLTVBGENAVITTCNGSGPLPDVD 242
Qy 230 MDVGNLVS-----KHNMTSHTQSLRITNISDDSGKQISCAENLVGEDODSVNLTVA 284
Db 243 MIVTGLQSIHTHOTNLMTNVAHNLTLVNTSBDNGLFLTCLAENVGSMNSVALLTVH 302
Qy 285 PAFITTFLESPTSDHMCIPFTVKGPNKPAQWFNGAALINESKYICTKIHVTNHTBYH- 343
Db 303 YPRPVVLSLEPELRLEHCIFEVVKGPNPPTLHMLHNGQVLRREK-----ITHVAYYQ 354
Qy 344 ---GCLQDLPNTNMGDYLTLAKNEYCKDEKQISAPFMGPGIDGDANPVYD-----FPE- 403
Db 355 EGVSEGCCLLFNKPRTNHNNGYITVAITNQLASANTQIKGHLEXP-----FPE--S 403
Qy 398 EDVYGTANDIGDTNRSNEIPSTDVTDKTRGHEHLSVAAVVIASVVGFC-LIYMLFLL-- 454
Db 404 TDNFVSFEYVSP-----PRTVTHKREBDTFCGSIANGLAFA--CYLLVVLFFIMIN 454
Qy 455 KLARHSKFGMKGPASVISNDSDASPLHH-----ISNGSNTSSSEGGPDAVIIGMT 506
Db 455 KYGRRSKFGMKGPVAVISGEBDSASPLHNDQPMHHTLITGRBAGH-----VIGMT 506
Qy 507 KIPPIENPQYFGITNSQLKBDTPVOHKKRNIVYLRKELGAGRGKVLACNYLCPRODK 566

```


Db 507 RPIVENPQYRGCHNCCKPPTYOHIKRRDVLKRELGEGAFGVFLAECYNLSPIYVK 566
 QY 567 ILVAVKTLKDSADNARKDFHREAEILLTNLOHEHLYKFGVCEGDPPLIMEYMKGDIN 626
 Db 567 MLVAVKOLKDPFLAARQDFGAEELLTNLOHEHLYKFGVCGDDPPLIMVEYMKHGLN 626
 QY 627 KFLRAHGDPAVLMAEGND--PTEITQSOMLHIAOQIAAGVYLASQHFVRDLATRNCL 683
 Db 627 KFLRAHGDPAVLMAEGND--PTEITQSOMLHIAOQIAAGVYLASQHFVRDLATRNCL 686
 QY 684 VGENLLVYKIGDPMGRSDYSTDYRVGHTMLPIRMMPESIMYRKFTTESDWSLSGLVL 743
 Db 687 VGANLVVIGDPMGRSDYSTDYRVGHTMLPIRMMPESIMYRKFTTESDWSLSGLVL 746
 QY 744 WEITFYGQPMYQLSNNVEICTQGRYLQRPCTQPOVEYELMGCMQREPMRNKNGI 803
 Db 747 WEITFYGQPMYQLSNNVEICTQGRYLQRPCTQPOVEYELMGCMQREPMRNKNGI 806
 QY 804 HTLLQNLAKASPVYLDILG 822
 Db 807 YKILHALGKATPIYLDILG 825

RESULT 13

S35695
 neurotrophin-3 receptor precursor - chicken
 N:Alternate names: receptor tyrosine kinase trkc
 N:Contains: protein-tyrosine kinase (BC 2.7.1.112)
 C:Species: Gallus gallus (chicken)
 C>Date: 10-Dec-1993 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
 C:Accession: S35695
 R:Okazawa, H.; Kamei, M.; Kanazawa, I.
 FEBS Lett. 329, 171-177, 1993
 A:Title: Molecular cloning and expression of a novel truncated form of chicken trkc.
 A:Reference number: S35695; MUID:93359043; PMID:8394830
 A:Accession: S35695
 A:Molecule type: mRNA
 A:Residues: 1-803 <OK>
 A:Cross-references: UNIPROT:O91044; EMBL:X59669; NID:9416429; PIDN:CAA42202.1; PID:94164
 C:Note: the authors translated the codon AAC for residue 105 as Val, CIG for residue 108
 C:Function: regulation of nervous system development; receptor for neurotrophin-3
 C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycop
 C:Keywords: alternative splicing; ATP; autophosphorylation; brain; glycoprotein; growth
 ctein kinase
 F:1-10/Domain: signal sequence #status predicted <SIG>
 F:11-803/Product: neurotrophin-3 receptor #status predicted <MAT>
 F:11-417/Domain: extracellular #status predicted <EXT>
 F:58-82/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
 F:83-106/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F:107-129/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 F:130-141/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR
 F:418-434/Domain: transmembrane #status predicted <TM>
 F:435-803/Domain: cytosolic #status predicted <CT>
 F:514-795/Domain: protein kinase homology <KIN>
 F:522-530/Region: protein kinase ATP-binding motif
 F:47-51,58,142,182,197,211,238,246,251,273,354,367/Binding site: carbohydrate (Aam) (cov
 F:550/Active site: Lys #status predicted
 F:687/Binding site: phosphate (Tyr) (covalent) #status predicted
 F:798/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 48.6%; Score 2149.5; DB 1; Length 803;
 Best Local Similarity 53.3%; Pred. No. 1.7e-95;
 Matches 448; Conservative 112; Mismatches 202; Indels 79; Gaps 18;
 QY 19 CMLVGFWRAPACPTSCSKSASRIWCSDPSPGIVAPRLRP-----NSVD-P 65
 Db 5 CMRIFFASRLKLVLFKTD-----INCKKDDGNL-PFLLEGDSGSSNGMTSINITDIS 56
 QY 66 ENRIEIFLANOKKLEINEDVEAVGIRNLITYDSGLKFAHAKFLKNSMLQHNINFRN 125
 Db 57 RNITSIHENKMNQTLNAVMEIYTGRLTIRNSGLRNIOQRAFGNPHLRVYDLSGN 116

QY 126 KLTSLSKRHRRLDLSELILVGNPFTGSCDIMWIKTLQE-AKSSPDQDLCLNBSSKNI 184
 Db 117 RLTLTSMQLFQTLFLFDRLERPNFNCSDIRWIQLOKEKCANLQSQQLHGMULDVAVI 176
 QY 185 PLALQIPNCGLPBANLAAPLTYEBKSLITLGSVAGDPVPMYVGNLVS-----KH 239
 Db 177 LLRRMNTQDCDLPESVSHVNLTVREGENAVITNCGSSPLPDVDVADLHLSINTQTN 236
 QY 240 MNETSHTQGSILRTINISDSDGKQISGVAENLVGEDDSDVNLVTHAFPTITFLSPSTDH 299
 Db 237 LMTNVAINILTVNVTSEDNGLFTTCAENVGMASAVLLTYYPRIITLLEPVHL 296
 QY 300 HMCIPFTVKNPKPALQMFNGAILNESKYLCTKIHTNTHY-----GCLQDNPT 352
 Db 297 EHCIAFVHGNPAPLTLMLHNGQVLRTEII-----HMEFYQGEVSGCLLPNKP 348
 QY 353 HNNNGDTLLAKNEYGDEKQISAHFMGMFGCIDGGAAPNYD-----VIYEDYGTANDI 407
 Db 349 HNNNGDTLLAKNEYGDEKQISAHFMGMFGCIDGGAAPNYD-----VIYEDYGTANDI 394
 QY 408 GDTTNRSNELPSTVDTPDKTGREHLSYAVVYASVGFCLLNLVFL--KLARHSKRG 464
 Db 395 SPT-----PRTVTKRPEEDTGVSAVGLAFA--CVLLVFLTINKYGRSRKGM 445
 QY 465 KGPASVLSNDDASAPLHHSNGSNTPSSSEGGDAVIGMTKLPVENPQYFGITNSQL 524
 Db 446 KGPVAVISGEEDSAAT--HTST-TDTRFVTDAGDVTIVGTRLPVENPQYFGQHCH 502
 QY 525 KPDTFVOHKKRNLVLRKELGEGAFGVFLAECNLCPEODKILVAVKTLKDSADNARKD 584
 Db 503 KPDTFVOHKKRNLVLRKELGEGAFGVFLAECNLCPEODKILVAVKTLKDSADNARKD 562
 QY 585 FHRRAEILLTNLOHEHLYKFGVCEGDPPLIMVPEYMGHGDNKFRAHGPVAPVLAGNP 644
 Db 563 FHRRAEILLTNLOHEHLYKFGVCEGDPPLIMVPEYMGHGDNKFRAHGPVAPVLAGNP 622
 QY 645 ---PTELTQSOMLHIAOQIAAGVYLASQHFVRDLATRNCLVGENLLVYKIGDPMGRSDV 701
 Db 623 RQAKGELGLSQMLHIAQIASGMVYLASQHFVRDLATRNCLVGENLLVYKIGDPMGRSDV 682
 QY 702 YSTDYRVGHTMLPIRMMPESIMYRKFTTESDWSLSGLVLAEIFTYGQPMYQLSNNE 761
 Db 683 YSTDYRVGHTMLPIRMMPESIMYRKFTTESDWSLSGLVLAEIFTYGQPMYQLSNNE 742
 QY 762 VIECTQGRYLQRPCTQPOVEYELMGCMQREPMRNKNGIHTLLQNLAKASPVYLDIL 821
 Db 743 VIECTQGRYLQRPCTQPOVEYELMGCMQREPMRNKNGIHTLLQNLAKASPVYLDIL 802
 QY 822 G 822
 Db 803 G 803

RESULT 14

TRRTB
 nerve growth factor receptor precursor, high affinity - rat
 N:Alternate names: receptor tyrosine kinase trka
 N:Contains: protein-tyrosine kinase (BC 2.7.1.112)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C:Accession: A41981
 R:Meakin, S.O.; Suter, U.; Drinkwater, C.C.; Weicher, A.A.; Shooter, E.M.
 Proc. Natl. Acad. Sci. U.S.A. 89, 2374-2378, 1992
 A:Title: The rat trk proto-oncogene product exhibits properties characteristic of the s10
 A:Reference number: A41981; MUID:92196121; PMID:13127719
 A:Accession: A41981
 A:Molecule type: mRNA
 A:Residues: 1-799 <MEA>
 A:Cross-references: UNIPROT:P35739; GB:M85214; NID:9207481; PIDN:AAA42286.1; PID:9207482
 A:Note: sequence extracted from NCBI database (NCBI:88433, NCBI:88434)
 C:Comment: in Genbank entry RATTTRKRC, release 113.0, the source is designated as Rattus r
 C:Function: The proto-oncogene trka is activated by gene fusion. The amino end of several

A;Description: regulation of nervous system development; receptor for nerve growth factor
 C;Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycoprotein
 C;Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; phosphoprotein
 F;1-32/Domain: signal sequence #status predicted <SIG>
 F;33-799/Product: nerve growth factor receptor, high-affinity #status predicted <MAT>
 F;33-432/Domain: extracellular #status predicted <EXT>
 F;67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
 F;92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F;116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 F;139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LRR4>
 F;425-441/Domain: transmembrane #status predicted <TMN>
 F;442-799/Domain: cytosolic #status predicted <CYT>
 F;511-791/Domain: protein kinase homology <KIN>
 F;519-527/Region: protein kinase ATP-binding motif
 F;67,121,130,204,255,264,320,335,341,361,404/Binding site: carbohydrate (asn) (covalent)
 F;547/Active site: lys #status predicted
 F;663/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
 F;794/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 43.0%; Score 1901; DB 1; Length 799;
 Best Local Similarity 49.0%; Pred. No. 1,36-83;
 Matches 407; Conservative 112; Mismatches 254; Indels 58; Gaps 18;

QY 7 MHGPMARLMGFCMLVVGFWMAAFACPTSCSCAS-RWCSDBPGIAPRLEP-NSV- 63
 DB 12 WHRPA-----GLGLVTSMLA-----CACASCRCTCCPVGSGIRCTRACTLTLR 60
 QY 64 ---DPNTEIFINOKRLIINDDVAYVGLNLFTVDSGLRFVAKAFKLSNIOHI 120
 DB 61 GLRAGNLTLYVNGRDLQLEFEDQGLSLITVSGIAFLVAPDAHFRPRSHL 120
 QY 121 NFRNKLTSLSKRFRLDSELILVGNPFGSCDIMIKTL-GEANSPPTDLYCLNE 179
 DB 121 NLSNNALESLSMKTVQGLSLQDLTISGNPLHSCALMLQWQEDLCGVYTKLQSSGS 180
 QY 180 SSKRIPLANLQIPRCGLPSANLAPNLVTEGSKITLSCSASGDPVPMYMDVGNLYSKH 239
 DB 181 GDQFLPLQHNH--SCGVPSVVIQHPNOSVEKDDVFLQCVGQALQDADILTELGTGA 238
 QY 240 MNETSHTQGLRIT--NISDSGKQISCVLENLVGEODSVNLTVHPAPITFLASPTS 297
 DB 239 TMKSGDLPSGLTLVNTSLANKKNTCAENVDGARVSVQVSF-PASVHLGAWE 297
 QY 298 DHWCIPETVKNRPALQWFFNGALINSEKYICTKI---HYTNHTYHGLQADNPTM 354
 DB 298 QHMCIPPSVDGQAPSLRPFNGSVLNETSFIFLOFLESALTMTMHHGCLRINQPTHV 357
 QY 355 NNGVYTLIAKRYKDEKQISAHFMGWDGIDGANPNYEDYEDYGTAAINDGDTNRS 414
 DB 358 NNGVYTLIAANPYQAAASIMAAFM-----DNPEFNEDEIPVSPFV-----DTNSTS 407
 QY 415 NEISTDVTDTKGRBHLISVAVVIA--SVGFCLLVMLFLKLARSHKFGMGKSPASYISN 473
 DB 408 R-----DPEVKDETFPGVSAVGLAVALFLSALLVLVKKCGQRSLFGINRA--VLAP 461
 QY 474 DDDASPLMHSNNTPPSSSEGGPDAVILQMTKIPVLENPQYGTITNSQLKPTFYQHI 533
 DB 462 EDGLAMSLHFMITLGGSSLSPTKGGSG-----GHIEMENQYTS-----DTCVHI 508
 QY 534 KRNHIVLKRELGEAGFQVFLAECYNLCPEDDKILVAVKTLKASDNARKQFRRBAILT 593
 DB 509 KRQDIILLMELGEGAFQVFLAECYNLNDQDKMLVAKALKETSENARQDFHREBAILT 568
 QY 594 NLQHEHTYKFGVCSGSDPLIMVPEYMGSDPLNFKLHAGSDAVLMEGN--PPELTQS 651
 DB 569 MLDQHQHIVRFEGVCTBGGPLLVFETMKSHGDLNRLKSHGDAKLACGSDVAGPGLG 628
 QY 652 QMLTIAQOIAAGMYVLASQHFVHDLATRNCLVGENILVKIGDQMSRHYSTDYRVYG 711
 DB 629 QLLAVASVAAAGMYVLASLHFVHDLATRNCLVQSGLVVVKIGDQMSRDIYSTDYRVYG 688
 QY 712 HTMLPIRMPPESIMYRKFTTESDVWSLGVVLMELIFTYGKOPWQLSNNEVIECTQGRV 771

DB 689 RMLPIRMPPESILTRKSTESDVWSFGVVLMEIFTYGKOPWQLSNNTAIECTQGR 748
 QY 772 LQRPRTQPEVTELMGCMQREBPMRNKINGITLQLNLAKASPVYLDIIG 822
 DB 749 LBRPACPPPVVALMGCMQREBQQRISMVDVAPRLQALAAQAPPSYLDVIG 799

RESULT 15

TVRHTT
 Nerve growth factor receptor precursor, high affinity - human

N;Alternate names: receptor tyrosine kinase trkA
 N;Contains: protein-tyrosine kinase (EC 2.7.1.112)

C;Species: Homo sapiens (man)
 C;Date: 31-Dec-1988 #sequence, revision 30-Jun-1991 #text, change 11-Jun-1999

C;Accession: A30124; S02366; A25184
 C;Martin-Zanca, D.; Oskam, R.; Mitra, G.; Copeland, T.; Barbacid, M.

Mol. Cell. Biol. 9, 24-33, 1989

A;Title: Molecular and biochemical characterization of the human trk proto-oncogene.

A;Reference number: A30124; MUID:89181575; PMID:2927393

A;Accession: A30124

A;Residues: 1-790 <MAR1>
 A;Cross-references: GB:M23102; NID:9339917; PIDN:AAA6770.1; PID:9339918

R;Kozma, S.C.; Redmond, S.M.S.; Xiao-Chang, F.; Saurer, S.M.; Groner, B.; Hynes, N.B.
 EMBO J. 7, 147-154, 1988

A;Title: Activation of the receptor kinase domain of the trk oncogene by recombination w/
 A;Reference number: S00261; MUID:88196074; PMID:2966055

A;Accession: S02366

A;Molecule type: mRNA
 A;Residues: 393-758, 'HG', 761-790 <KO2>

A;Cross-references: EMBL:X06704; GB:T00100; NID:937399; PIDN:CAA29888.1; PID:937400
 R;Martin-Zanca, D.; Hughes, S.H.; Barbacid, M.

Nature 319, 743-748, 1986

A;Title: A human oncogene formed by the fusion of truncated tropomyosin and protein tyrosin
 A;Reference number: A25184; MUID:86146854; PMID:2869410

A;Accession: A25184

A;Molecule type: mRNA
 A;Residues: 393-762, 'SNATARMCTPGCKPMPRLHLSMTWMSMARPAQGLGVSRNTGACQHP' <MAR2>

A;Cross-references: EMBL:X03541; NID:937402; PIDN:CAA27243.1; PID:937403

A;Note: the difference at the carboxyl end is due to a frameshift

C;Comment: The proto-oncogene trkA is activated by gene fusion. The amino end of several

C;Genetics:

A;Gene: GDB:NTRK1; TRK
 A;Cross-references: GDB:127897; OMIM:191315

A;Map position: 1q21-1q22

A;Function:
 A;Description: regulation of nervous system development; receptor for nerve growth factor

C;Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycoprotein
 C;Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; phosphoprotein

F;1-32/Domain: signal sequence #status predicted <SIG>
 F;33-799/Product: nerve growth factor receptor, high-affinity #status predicted <MAT>

F;33-415/Domain: extracellular #status predicted <EXT>
 F;67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>

F;92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F;116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

F;139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LRR4>
 F;416-432/Domain: transmembrane #status predicted <TMN>

F;433-790/Domain: cytosolic #status predicted <CYT>
 F;502-782/Domain: protein kinase homology <KIN>

F;510-518/Region: protein kinase ATP-binding motif
 F;67,95,121,188,202,253,262,281,318,323,338,358,395/Binding site: carbohydrate (asn) (covalent)

F;538/Active site: lys #status predicted
 F;674/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

F;785/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 42.8%; Score 1893.5; DB 1; Length 790;
 Best Local Similarity 48.3%; Pred. No. 2,86-83;
 Matches 404; Conservative 116; Mismatches 228; Indels 79; Gaps 21;

QY 7 WH-----GPMARLMGFCMLVVGFWMAAFACPTSCSCASRHWCSDBPGIAPRLEPNS 62

Db 12 WHSWAGPSCI-----LAMLLASAGAA-PCPDAC-----CPHGSSGLRC---TRDGA 55
QY 63 VD-----PENTEIFIANOKRLEIINEDVEAYVGLRNLTVDSGLKFAVAKAFKNS 115
Db 56 LDSLHHLPGAENLTELVIENQOHQHLELRDLRGLGELRNLTIVKSGIRFAPAPDAFHFTP 115
QY 116 NLQHINFTRNKLTLSLRKHFRHLDLSLILVGNPFTCSCDIMWIKTL-QEAKSSPTQDL 174
Db 116 RLSRLNLSFVALBSLSWKTVOGLSLQELVLSGNPLHSCALRWLQRWEEBGLGVPQKL 175
QY 175 YCLNESSKNTPLANLQIPNGLPRSANLAAPLTYEBKSTILSGSVAGDPVPMNMYDVGN 234
Db 176 QCHGQG---PLAMPNASCGVPTLKQVQVPNASVDVGDVLLRCQVEGRGLEQAGWILTE 231
QY 235 LVSGHMETSHTOG-----SLRTNISSDSGKOISCAENLVGEDQSVNLTVHFAPTI 289
Db 232 L---EQSATYWKSGSLGLTLANVTSDLNRKNLTCHAEENDVGRAYSVQVNVSF-PAS 287
QY 290 TFLSPSTSDHHWCIPFTVKNPKPALQWFYNGAILNESKYICTKI--HVTNHTYHGCLQ 347
Db 288 VOLHTAVEMHMSIPFSVDGQAPASLRLWLFNGSVLNETSFIFTEFLBPAANETVRHGLR 347
QY 348 LDNPTNANGDYTLIAKNEYKDEKQISAHFMGWPIDGDNPNYPDYIYEDYGTANDI 407
Db 348 LNPETHVNNNGYTLAANPFQASASIMAFM-----DNPEFNPEDPIPTNSTS---- 398
QY 408 GDTNRNENIPSTVDTKGTGRENLSYAVVYVIAVSVGCLVLMFLKLAHSKFGKGP 467
Db 399 GDPVEKDETP-FGVSAVVG--LAVFACPLST-----LLVLNKGRRNKFGINRP 447
QY 468 ASVISNDSDSASPLHHSNPSSTSSSGPDAVIGMTKIPVLENPQYFGITNSQLKPD 527
Db 448 A-VLAPEDGLAMSLHFWTLGGSSLSPTBGKSGL-----QGHITENPOYFS-----D 493
QY 528 TFVOHITKRNIVLKRLEIGEGAFGVFLAECYNLCPEODKILVAVKTLKASDNARKDPR 587
Db 494 ACVHHIKRRDVLKMEIGEGAFGVFLAECYNLCPEODKILVAVKTLKASDNARKDPR 553
QY 588 EAEILLTNLOHEHIVKFGVCEGDPDLMVPEYMKHGDLNKLRAHGPDAVLMAGN--PP 645
Db 554 EAEILLTNLOHEHIVKFGVCEGDPDLMVPEYMKHGDLNKLRAHGPDAVLMAGN--PP 613
QY 646 TELTOSQMLHIAQOIAAGVYVIAQHFVHRDLATRNCLVGENLVLKIGDFGMSRDYSTD 705
Db 614 GPLGLGQLAVASQVAAQVYVIAQHFVHRDLATRNCLVGENLVLKIGDFGMSRDYSTD 673
QY 706 YRVVGHITMLPIRMWPPESIMYRKFTTESDVSLGVVLMELIFTYGQOPWYQLSNNEVIEC 765
Db 674 YRVVGHITMLPIRMWPPESIMYRKFTTESDVSLGVVLMELIFTYGQOPWYQLSNNEVIEC 733
QY 766 ITQGRVULQRPCTQOBYEELMLGCWOREPHNRKNIKGIHTLLQNLAKASPYLDILG 822
Db 734 ITQGRLEPRACPPEVYVIAIRGCMOREPQORHSIKDVHARLQALQAPVYLDVLG 790

Search completed: February 17, 2005, 00:28:19
Job time : 49 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 17, 2005, 00:06:11 ; Search time 25 Seconds
(without alignments)
1292.980 Million cell updates/sec

Title: US-10-645-546-2
Perfect score: 4419
Sequence: 1 MSSWIRHMGPMARLMGFCW.....IHTLLQNLAKSPYLDILG 822

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 154980 seqs, 39324206 residues

Total number of hits satisfying chosen parameters: 154980

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCF_NEM_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEM_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEM_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEM_COMB.pep:*
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6: /cgn2_6/ptodata/2/paa/US10_NEM_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US11_NEM_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/US60_NEM_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4162.5	94.2	821	1	PCT-US04-42360-2096 Sequence 2096, App
2	2296	52.0	825	1	PCT-US04-23166A-800 Sequence 800, App
3	2296	52.0	825	1	PCT-US04-42360-201 Sequence 201, App
4	2289	51.8	825	1	PCT-US04-23166A-657 Sequence 657, App
5	1901	43.0	799	1	PCT-US04-42360-293 Sequence 293, App
6	1263.5	28.6	337	1	PCT-US04-30360-81 Sequence 81, App1
7	1249	28.3	503	6	US-10-450-763-50636 Sequence 50636, A
8	763.5	17.3	502	1	PCT-US04-23166A-729 Sequence 729, App
9	756	17.1	345	1	PCT-US04-30360-82 Sequence 82, App1
10	722	16.3	985	6	US-10-450-763-47493 Sequence 47493, A
11	679.5	15.4	1367	6	US-10-937-758A-97 Sequence 97, App1
12	676	15.3	1370	6	PCT-US04-42360-862 Sequence 862, App
13	660	14.9	376	1	PCT-US04-30360-83 Sequence 83, App1
14	654	14.8	806	1	PCT-US05-00638-81 Sequence 81, App1
15	634	14.3	370	1	PCT-US04-30360-50 Sequence 50, App1
16	622	14.1	354	1	PCT-US04-30360-93 Sequence 93, App1
17	608.5	13.8	822	8	US-60-647-642-36 Sequence 36, App1
18	601	13.6	306	1	PCT-US04-30360-70 Sequence 70, App1
19	601	13.6	370	6	US-10-450-763-51309 Sequence 51309, A
20	601	13.6	675	6	PCT-US04-30360-29 Sequence 29, App1
21	596.5	13.5	299	1	US-10-450-763-51719 Sequence 51719, A
22	595.5	13.5	806	6	PCT-US04-42360-604 Sequence 604, App
23	590	13.4	1114	1	PCT-US04-23813-4 Sequence 4, App1
24	589	13.3	983	1	PCT-US04-06979-467 Sequence 467, App
25	589	13.3	983	1	PCT-US04-06979-467 Sequence 467, App

26	589	13.3	983	6	US-10-794-514A-467 Sequence 467, App
27	578	13.1	986	8	US-60-646-841-30 Sequence 30, App1
28	578	13.1	997	6	US-10-450-763-36048 Sequence 36048, A
29	578	13.1	1026	6	US-10-450-763-53290 Sequence 53290, A
30	565.5	12.8	485	7	US-11-033-545-525 Sequence 525, App
31	565.5	12.8	803	7	US-11-033-545-340 Sequence 340, App
32	560	12.7	384	1	PCT-US04-30360-68 Sequence 68, App1
33	558	12.6	373	1	PCT-US04-30360-68 Sequence 68, App1
34	557	12.6	947	6	US-10-450-763-52541 Sequence 52541, A
35	555	12.6	1338	7	US-11-021-951-114 Sequence 114, App
36	555	12.6	1421	6	US-10-450-763-36458 Sequence 36458, A
37	551.5	12.5	1089	6	US-10-450-763-51112 Sequence 51112, A
38	544	12.3	379	1	PCT-US04-30360-45 Sequence 45, App1
39	537	12.2	310	1	PCT-US04-30360-27 Sequence 27, App1
40	537	12.2	388	6	US-10-450-763-50983 Sequence 50983, A
41	536	12.1	312	1	PCT-US04-30360-41 Sequence 41, App1
42	531.5	12.0	987	6	US-10-938-061-100 Sequence 100, App
43	531.5	12.0	987	6	US-10-936-626-100 Sequence 100, App
44	528.5	12.0	343	1	PCT-US04-30360-57 Sequence 57, App1
45	525	11.9	986	6	US-10-938-061-101 Sequence 101, App

ALIGNMENTS

RESULT 1
PCT-US04-42360-2096
Sequence 2096, Application PC/TUS0442360
GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation doing business as Massachusetts General
APPLICANT: Hospital / Bayer AG
TITLE OF INVENTION: Nucleotide sequences involved in pain
FILE REFERENCE: 17633/2048
CURRENT APPLICATION NUMBER: PCT/US04/42360
CURRENT FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: 60/531,341
PRIOR FILING DATE: 19-Dec-2003
NUMBER OF SEQ ID NOS: 2587
SOFTWARE: Perl script
SEQ ID NO 2096
LENGTH: 821
TYPE: PRT
ORGANISM: Rattus norvegicus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Refseq / NP_036863
DATABASE ENTRY DATE: 2003-10-06
PCT-US04-42360-2096
Query Match 94.2%, Score 4162.5, DB 1, Length 821;
Best Local Similarity 93.6%, Pred. No. 8e-245;
Matches 769; Conservative 25; Mismatches 27; Indels 1; Gaps 1;
QY 1 MSSWIRHMGPMARLMGFCWLVGFWRAAFACPTSCCKSASRIWCSDPSPGIVAFPRLEP 60
1 MSMPWRHMGPMARLMGFCWLVGFWRAAFACPTSCCKSASRIWCSDPSPGIVAFPRLEP 60
DB 1 MSMPWRHMGPMARLMGFCWLVGFWRAAFACPTSCCKSASRIWCSDPSPGIVAFPRLEP 60
QY 61 NSVDPNTEFFINOKRELIINEDDVEAYVGLNLTIVDSGLKFWAHKALKXSNLOHI 120
61 NSIDPENITELLINOKRELIINEDDVEAYVGLNLTIVDSGLKFWAHKALKXSNLOHI 120
DB 61 NSIDPENITELLINOKRELIINEDDVEAYVGLNLTIVDSGLKFWAHKALKXSNLOHI 120
QY 121 NPTNKLTSLSRKAFRRHLDSELIIVGNPFTSCSDIMWIKTLQBAKSSPDQDLYCLNBS 180
121 NPTNKLTSLSRKAFRRHLDSELIIVGNPFTSCSDIMWIKTLQBAKSSPDQDLYCLNBS 180
DB 121 NPTNKLTSLSRKAFRRHLDSELIIVGNPFTSCSDIMWIKTLQBAKSSPDQDLYCLNBS 180
QY 181 SKNPLANLQIPNCGLPBANLAAFNLTVEBKSITLSCSVAGDPVPMNYDGNLVSRGM 240
181 SKNPLANLQIPNCGLPBANLAAFNLTVEBKSITLSCSVAGDPVPMNYDGNLVSRGM 240
DB 181 SKNPLANLQIPNCGLPBANLAAFNLTVEBKSITLSCSVAGDPVPMNYDGNLVSRGM 240
QY 241 NETSHTOGSLRITITSSDDSGKQISCVABNIVGSDQSVNLTVHAPITTLSEPTSDH 300
241 NETSHTOGSLRITITSSDDSGKQISCVABNIVGSDQSVNLTVHAPITTLSEPTSDH 300
DB 241 NETSHTOGSLRITITSSDDSGKQISCVABNIVGSDQSVNLTVHAPITTLSEPTSDH 300
QY 301 WCIPFTVGNPKPALQWFFYNQALINSEKYICTKIHVTHTYHGCLOLDNPTHMNGDYT 360
301 WCIPFTVGNPKPALQWFFYNQALINSEKYICTKIHVTHTYHGCLOLDNPTHMNGDYT 360

Db	301	WCIFFTYRGNDKPALQWYFNCAIILNBSKXICIKIKHVHTHTTEYHGLQJQDNTFTTHMNGDYT	360
Qy	361	LIANREYKDEKQJISAHPMGWPGIDDGANEVTPDYIVEDYGTANDIGDTNRSNEIPST	420
Db	361	LMANREYKDEKQJISAHPMGWPGVDYENPNPYEVLVEDW-TTPDIDIDITNKSNEIPST	419
Qy	421	DVDTKGTGRENHSYAAVVVIASVWGCLVLMFLKLGDAHSFKMGKGPASVISNDDSDASP	480
Db	420	DVAQQTREHLSYAAVVVIASVWGFCCLVMLLLKLKLAHSFKMGKGPASVISNDDSDASP	479
Qy	481	LHHSINSGNTSSSBGPDVAIIGMTKIPVIENPPQYFGITNSQLKPDTFVOHKIKHNVL	540
Db	480	LHHSINSGNTSSSBGPDVAIIGMTKIPVIENPPQYFGITNSQLKPDTFVOHKIKHNVL	539
Qy	541	KREIGEGRGKVFPLAECNLCPEODKILVAKTKLQDASDNARKDPHRAEELLTMQHSHI	600
Db	540	KREIGEGRGKVFPLAECNLCPEODKILVAKTKLQDASDNARKDPHRAEELLTMQHSHI	599
Qy	601	VKIFYGVCSBGPPLIVFEFYMKGDLNKFILRAHGPDAVMAEGNPTELTOSOMLHIAOI	660
Db	600	VKIFYGVCSBGPPLIVFEFYMKGDLNKLRAHGPDAVMAEGNPTELTOSOMLHIAOI	659
Qy	661	AAGWVYLAHQFVHDLATRNCLVGENLLVKIGDFGMSRDVYSTDYEVGHTMLPIRMM	720
Db	660	AAGWVYLAHQFVHDLATRNCLVGENLLVKIGDFGMSRDVYSTDYEVGHTMLPIRMM	719
Qy	721	PPESIMRKFTTESBQWMSLGYVLMEIFTYGQOPWQLSNNEYICITQGRVLORPRTCPQ	780
Db	720	PPESIMRKFTTESBQWMSLGYVLMEIFTYGQOPWQLSNNEYICITQGRVLORPRTCPQ	779
Qy	781	EVEYELMGCMQREPHMRKINIGIHTELONLAKASPVYLDILG	822
Db	780	EVEYELMGCMQREPHMRKINIGIHTELONLAKASPVYLDILG	821
RESULT 2			
PCT-US04-23166A-800			
Sequence 800, Application PC/TUS0423166A			
GENERAL INFORMATION:			
APPLICANT: Purdue Pharma L.P.			
APPLICANT: Jiefei Tong			
APPLICANT: Gang Jin			
APPLICANT: Rui-Ju Ji			
APPLICANT: Yixun Xu			
APPLICANT: Lillian W. Chiang			
TITLE OF INVENTION: GENES ASSOCIATED WITH RESPONSES TO NEUROPATHIC PAIN			
FILE REFERENCE: 02755/200M584-WO0			
CURRENT FILING DATE: 2004-07-06			
PRIOR APPLICATION NUMBER: 60/485,101			
PRIOR FILING DATE: 2003-07-03			
NUMBER OF SEQ ID NOS: 868			
SOFTWARE: PatentIn version 3.1			
SEQ ID NO 800			
LENGTH: 825			
TYPE: PRT			
ORGANISM: Rattus norvegicus			
PCT-US04-23166A-800			

Query Match 52.0%; Score 2296; DB 1; Length 825;
 Best Local Similarity 55.0%; Pred. No. 9,4e-132;
 Matches 468; Conservative 107; Mismatches 206; Indels 70; Gaps 16

QY 10 PAMARLW-----GFCWL-VGCFMRAAFCAPTSCSKSASRIWCDSPGIVAFPRLEP--- 60
 Db 7 PAKCSFWRIFPLLGSGVMDLYVG---SVLCAFPANCVCSTKEINRRRDDGNTL-FPLLEGQDS 62

QY 61 -----NSVD--PENTTEIFIANQKLEIINEDDVAAYVGLRRLTIVDSGLKRVAKHA 110
 Db 63 GNSGNMASINTTDSRNITSHIENWRGLHTINAVDMELVYGLQKLTINKSGLRNTIQPRA 122

Qy	11	PLKNSUHQINPTKTKTSLSKPHRDLSELLVGNPFCSDIMWITLQG-AASSP	169
Db	123	FAKNPHKRTINSNRLLTTLSSQOLFQTLISLBLELQNFQCSDDIMQJMGQEARL	182
Qy	170	DTQDLYCLINBSSKNIPLANLOIPNGCLPSANLAAPNITVEGKSITLSCSVADPVPNMV	229
Db	183	DSQSLYICISADSOQLPFRPMNISQCDLPBISVSHVNLITVEBGDAVAVITTCNGSGSLPDPD	242
Qy	230	KWQVGNLVS-----KMNETHSQGSLRTNISSPDQSKQISCVAEENLVGBDQSVNLTYH	284
Db	243	WYTGQSINTHQTNLMTNVAHNLNLVNTSBDNGTTLCLABENVGMSNVALTYV	302
Qy	285	FATTIFLESPTSDHMCIPFTVKGNPKPALOMFYNGALINBESKYICTKLIHTVNHTESYH-	343
Db	303	YPRPVSLVPEBVRLEHCLIEFYVGNRPFTPLHMLTNQPLRESKLTI-----HMDYQ	354
Qy	344	-----GCLQDNDPTHMNGDYTLIAKNEYKDEKQISAHFPMWPGIDGAPNPYDVIY	397
Db	355	EGEVBGCLLFNKPPTHYNNGNVTLIAKVALGTANQINGHFLKSP-----PFE---	402
Qy	398	EDYGTANDIGTTKRSNEIPSTDYDTKTGEBHLSYAVAVVIVASVQFC-LYMLFL--	454
Db	403	-----STPFFBESDASPTPEITVYTHRBSDDTGVSLAVGLAFA--CVLLVLFPMIN	454
Qy	455	KLARSKFQMKQRPASVINSDDDSASPLKHIINSNSTPSSSEGGDAVYIGMTKXIPVLENP	514
Db	455	KYGRNSKFKMKQRPAAVISEEDSASPLHINHGTITBSSLDAGDVIYIGMTKXIPVLENP	514
Qy	515	OYFGITNSQLKPDTFVOHIKRANIVLKELEBGAFGKVFALBCYNLCPEQDKILVAVKTL	574
Db	515	QYRQGHCHKQDVTYVQHIKRQDYLAKLELGBAGFGKVFALBCYNLSPTKQKMLVAVKAL	574
Qy	575	KDASDNARQDFREABLLTNLOHEHITVYFYGVCVBGDPILNVFPTMKGDLAKFLRAHP	634
Db	575	KQPTLAAARDFORABELLTNLOHEHITVYFYGCDGDPILNVFPTMKGDLAKFLRAHP	634
Qy	635	DAYLMAEGNP-----PTELQSQMKLTAQOIIAAGVYVLASQHFVHDLATRCJLGENMLVYK	691
Db	635	DANILVDGQPRQAKSELGISQMLHIASQIASGAMVYVLASQHFVHDLATRCJLGVANMLVYK	694
Qy	692	IGDFGMSRUVSSTDYVYRVOGHMTLPIRMMPPESSIMYRKFTTESDVMSLGVLMIEPTYGK	751
Db	695	IGDFGMSRUVSSTDYVYRVOGHMTLPIRMMPPESSIMYRKFTTESDVMSEFVILMEIPTYGK	754
Qy	752	QRPYQLSNNEVIECTTQGRVLORPPTCQSBYBELMLGCMQREBPMKQIKIGIHTLQNLTA	811
Db	755	QPFQJSLNSTEVEICTQGRVLERPEVCBEKAYDMLGCMQREBPMKQIKIGIHTLQNLTA	814
Qy	812	KASPVYLDILG	822
Db	815	KATPIYLDILG	825

```

RESULT 3
PCT-US04-42360-201
: Sequence 201. Application PC/RTUS0442360
:
: GENERAL INFORMATION:
: APPLICANT: The General Hospital Corporation doing business as Massachusetts General
: APPLICANT: Hospital / Bayer AG
: TITLE OF INVENTION: Nucleotide sequences involved in pain
: FILE REFERENCE: 17633/2048
: CURRENT APPLICATION NUMBER: PCT/US04/42360
: CURRENT FILING DATE: 2004-12-17
: PRIOR APPLICATION NUMBER: 60/531,341
: PRIOR FILING DATE: 19-Dec-2003
: NUMBER OF SBO ID NOS: 2587
: SOFTWARE: perl script
: SBO ID NO 201
:
: LENGTH: 825
:
: TYPE: FRT
: ORGANISM: Rattus norvegicus
: PUBLICATION INFORMATION:
: DATABASE ACCESSION NUMBER: Refseq / NP_062121

```

DATABASE ENTRY DATE: 2003-10-06
PCT-US04-42360-201

Query Match 52.0%; Score 2296; DB 1; Length 825;
Best Local Similarity 55.0%; Pred. No. 9,4e-133;
Matches 468; Conservative 107; Mismatches 206; Indels 70; Gaps 16;

10 PAMARLW-----GFCWL-VGFWRAAFACPTSCCKSASRIWCDSPSPGIVAPRLP--- 60
7 PAKSFWRIPLGSLVWLDYVG---SVLACPANVCVSKTEINCRPRDDGNL-FPLLEGDS 62
61 -----NSVD-PENITEIFIANOKRLEIINEDVEAYVGLRLTIVDSGLKFAVAKA 110
63 GNSGNASINTIDSRNITSIHENWRGLHTLNAVDMELVGLQKLTIKNSGLRNIOGRA 122
111 FLKNSNLQHINFTNRKLTSLRKPRHLDELIVGNPFCSCDIMWIKTLQF-AKSSP 169
123 PAKPHRLRYINLSNRILTLTSWOLFOTLSRELBLEONFNCSCDIRMQLMOEGEAKL 182
170 DTODLYCLNESSKNIPLANLOIPNCGLPANLAAPNLTVEBKSITLSCSVAGDPVPMY 229
183 DSQSLYCSADGSQLPFRMNISQCDLPEISVSHNLTVRBGDAVITCNGSSGPLPVD 242
230 WDVGNLVS-----KHNETSHTQSLRITNISSDSKQISCVANLVGEDQDSVNLTVH 284
243 WIVTGLQSIHTQTNLMNTVHAINLTLVNTVSEDNFTLTICIAENVVGMNASVALTVY 302
285 FAPITTLFLESTSHHNCIPFTVYKGNPKRALQWFTNGALINESKYICTKIHVHTNTEH- 343
303 YPRVSVLSIEBEVRLERHCIEFVVRGNPPTLHMLNQGPLEBSKI-----HMDYQ 354
344 -----GCLQDNPTNHNNGDYTLIAKNEYGKDEKOISAHFMGPGIDDGANPNVDPVY 397
355 EGEVSEGLLNKPKPTHYNNNGYTLIAKALSTANQTINGHFLKEP-----PPE--- 402
398 EDYGTAAANDIGDTTNRSEIPESTDVDTKGRBHLSVYAVVIAVVGFC-LVLMFL- 454
403 -----STDFPESDASPTPEITVTYHKREEDTFGVSIAVGLAFA--CVLLVVLFIWIN 454
455 KLARHSKFGMKGPASVISNDSDASPLHINSNSTPSSSEGGPDAVITGMTKIPVLENP 514
455 KYGRSRKFGMKGPAAVVISGEEDSASPLHINHGITTPSSLDAGPDTVVIGMTRIPIVLENP 514
515 QYFGITNSOLKPDFTVOHIKRHNIVLKRELEGAFAKGFYLAECYNLCPEODKXIVAVTIL 574
515 QYFPGHNCCHKPDYTVQHKRDIVLKRELEGAFAKGFYLAECYNLCSTKXMLVAVKAL 574
575 KQASDNARKDFRREABLLTNLOHEHIVKFGYCVGEGDPLINVFEMKHDINKFLRAHGP 634
575 KQPLTAAKDFRREABLLTNLOHEHIVKFGYCVGEGDPLINVFEMKHDINKFLRAHGP 634
635 DAVILABGNP---PTELTSQOMLHTAQOIAAGMYTLASQHFVHRDLATNCLVGENLIVK 691
635 DAVILVVGQPRQAKGELISQMLHTASQIASGMVYTLASQHFVHRDLATNCLVGENLIVK 694
692 IGDGMSRDVYSTDYVRVGGHTMLPIRMWPESIMYRKFTTESDWSLGVLMELFTYTGK 751
695 IGDGMSRDVYSTDYVRVGGHTMLPIRMWPESIMYRKFTTESDWSLGVLMELFTYTGK 754
752 QPWTQLSNNEYIECTTQGRVLAQRPRTCPQEVYELMCMQREPHMKRIKIGITHTLQVLA 811
755 QPWQOLSTEVIECTTQGRVLAQRPRTCPQEVYELMCMQREPHMKRIKIGITHTLQVLA 814
QY 812 KASPEYLDITG 822
Db 815 KATPIYLDITG 825

RESULT 4
PCT-US04-23166A-657
Sequence 657, Application PC/TUS0423166A
GENERAL INFORMATION:
APPLICANT: Purdue Pharma L.P.

APPLICANT: Jiefei Tong
APPLICANT: Gang Jin
APPLICANT: Rui-Ru Ji
APPLICANT: Yixun Xu
APPLICANT: Yixun Xu
APPLICANT: Lillian W. Chiang
APPLICANT: Daniel J. Lavery
TITLE OF INVENTION: GENES ASSOCIATED WITH RESPONSES TO NEUROPATHIC PAIN
FILE REFERENCE: 02755/200M584-MO0
CURRENT APPLICATION NUMBER: PCT/US04/23166A
CURRENT FILING DATE: 2004-07-06
PRIOR APPLICATION NUMBER: 60/485,101
PRIOR FILING DATE: 2003-07-03
NUMBER OF SEQ ID NOS: 868
SOFTWARE: PatentIn version 3.1
SEQ ID NO 657
LENGTH: 825
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US04-23166A-657

Query Match 51.8%; Score 2289; DB 1; Length 825;
Best Local Similarity 54.4%; Pred. No. 2,5e-131;
Matches 466; Conservative 111; Mismatches 199; Indels 80; Gaps 17;

10 PAMARLW-----GFCWL-VGFWRAAFACPTSCCKSASRIWCDSPSPGIVAPRLP--- 60
7 PAKSFWRIPLGSLVWLDYVG---SVLACPANVCVSKTEINCRPRDDGNL-FPLLEGDS 62
61 -----NSVD-PENITEIFIANOKRLEIINEDVEAYVGLRLTIVDSGLKFAVAKA 110
63 GNSGNASINTIDSRNITSIHENWRGLHTLNAVDMELVGLQKLTIKNSGLRNIOGRA 122
111 FLKNSNLQHINFTNRKLTSLRKPRHLDELIVGNPFCSCDIMWIKTLQF-AKSSP 169
123 PAKPHRLRYINLSNRILTLTSWOLFOTLSRELBLEONFNCSCDIRMQLMOEGEAKL 182
170 DTODLYCLNESSKNIPLANLOIPNCGLPANLAAPNLTVEBKSITLSCSVAGDPVPMY 229
183 NSQMLYCLINDGSQLPFRMNISQCDLPEISVSHNLTVRBGDAVITCNGSSGPLPVD 242
243 WIVTGLQSIHTQTNLMNTVHAINLTLVNTVSEDNFTLTICIAENVVGMNASVALTVY 302
230 WDVGNLVS-----KHNETSHTQSLRITNISSDSKQISCVANLVGEDQDSVNLTVH 284
243 WIVTGLQSIHTQTNLMNTVHAINLTLVNTVSEDNFTLTICIAENVVGMNASVALTVY 302
285 FAPITTLFLESTSHHNCIPFTVYKGNPKRALQWFTNGALINESKYICTKIHVHTNTEH- 343
303 YPRVSVLSIEBEVRLERHCIEFVVRGNPPTLHMLNQGPLEBSKI-----HVEYQ 354
344 -----GCLQDNPTNHNNGDYTLIAKNEYGKDEKOISAHFMGPGIDDGANPNVDP- 394
355 EGEISBGLFNKPTHYNNNGYTLIAKALSTANQTINGHFLKEP-----PPESTD 405
395 --VIEDYGTAAANDIGDTTNRSEIPESTDVDTKGRBHLSVYAVVIAVVGFC-LVLMFL 451
406 NFILFBEV-----SPTPEITVTYHKREEDTFGVSIAVGLAFA--CVLLVVL 449
452 FL--KLARHSKFGMKGPASVISNDSDASPLHINSNSTPSSSEGGPDAVITGMTKIP 509
450 FVMINKYGRSRKFGMKGPAAVVISGEEDSASPLHINHGITTPSSLDAGPDTVVIGMTRIPI 509
510 VTEPNQYFGITNSOLKPDFTVOHIKRHNIVLKRELEGAFAKGFYLAECYNLCPEODKXIV 569
510 VTEPNQYFGITNSOLKPDFTVOHIKRHNIVLKRELEGAFAKGFYLAECYNLCSTKXMLV 569
570 AVKTLKQASDNARKDFRREABLLTNLOHEHIVKFGYCVGEGDPLINVFEMKHDINKFL 629
570 AVKTLKQPLTAAKDFRREABLLTNLOHEHIVKFGYCVGEGDPLINVFEMKHDINKFL 629
630 RAHGPDAVILABGNP---PTELTSQOMLHTAQOIAAGMYTLASQHFVHRDLATNCLVGE 686
630 RAHGPDAVILVDDQPRQAKGELISQMLHTASQIASGMVYTLASQHFVHRDLATNCLVGA 689
687 NLVVKIDFGMSRDVYSTDYVRVGGHTMLPIRMWPESIMYRKFTTESDWSLGVLMEL 746

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Db      690 NLVVKIDFGMSRNVSTDYRRVGHTMLPIRMPPESIMRKTTSSDVSFVILMEI 749
Qy      747 FTYGKQPMYQLSNNEVEICTGGVLTORPTCPQEVYELMGCMQREPHMKIKIHLL 806
Db      750 FTYGKQPMYQLSNNEVEICTGGVLTORPTCPQEVYELMGCMQREPHMKIKIHLL 809
Qy      807 LQNLAKASPVYLDILG 822
Db      810 LHALGKATPIYLDILG 825

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RESULT 5

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PCT-US04-42360-293
; Sequence 293, Application PC/TUS0442360
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: 17633/2048
; CURRENT APPLICATION NUMBER: PCT/US04/42360
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: 60/531,341
; PRIOR FILING DATE: 19-Dec-2003
; NUMBER OF SEQ ID NOS: 2587
; SOFTWARE: Perl script
; SEQ ID NO 253
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; ORGANISM: INFORMATION:
; DATABASE ACCESSION NUMBER: Refseq / NP_067600
; DATABASE ENTRY DATE: 2003-10-05
PCT-US04-42360-293

```

Query Match 43.0%; Score 1901; DB 1; Length 799;

Best Local Similarity 49.0%; Pred. No. 7,66-108; Matches 407; Conservative 112; Mismatches 254; Indels 58; Gaps 18;

```

Qy      7 WHGPMARLWGCWLVVGFWRAPAFACPTSCSKSAS-RIMSGDPSPGIAPRRLRP-NSV- 63
Db      12 WHRPAA-----GLGGLVYSLMLA-----CACASCBETCCPVPSPGLRTRAGTLNLTLR 60
Qy      64 ----DPEVITETFINQKRLIINDDYEAIVYGLNLTIVDSGLKFAVHAKAFKLSNIOHT 120
Db      61 GLRGAGVLTLYVQNRDLQRLREDFDQGLQELSLTIVYSGLRFVAPDAFHFTPRLSHL 120
Qy      121 NFRNKLTSLSRKFRHLDSELIVGNPFTSCDIMMIKTL-QEAKSSPTODLYCLNE 179
Db      121 NLSNNALESLSKTVQGLSLDGLTSLGNPLHSCALMLQMEQBDLCGYTTQKLGSGS 180
Qy      180 SSKNIPLANLQIPNCGLPSSANTLAAPNLVEBKSITLSCVAGDPVPMYMDVGNLVSKH 239
Db      181 GDQVPLGHNH--SCGVPSVKIQMPNDSEVGVDDVPLQCVBGAALQADWILTELESGTA 238
Qy      240 MNEISHQSGSRIT--NISDPSGKQISCVAKENLYGBDQDSVNLTPAPATITTLSEBPTS 297
Db      239 TMKSGDLPISGLTLYVNTSDLNKKNYTCVAKENLVGAHSVQVSVF-PASVHLGAVVE 297
Qy      298 DHHHCIPFYVGNKRPALQWYNGAILNESKYICPKI---HTVHTHEVHGLQLDNPTM 354
Db      298 QHHHCIPFVSVDGQAPSLKMFNFNSVLANETSFITQPLBSALNTEHMGRLNQPTHV 357
Qy      355 NNGDYTLIAKNBYKDEKQISAHFMGPGIDGAPNYPDVLYEDYGTAAIDGTTNRS 414
Db      358 NNGDYTLIAANPYQGAASIAAFM-----DNPEFNPEDPIPVSPSV-----DTNSTS 407
Qy      415 NEISTVTDYKTEGHHLSYAVVVI--SVGFCLVIMFLIAKLARSHKFGKGPASYISN 473
Db      408 R-----DPVEKKDETPFGVSAVGLAVSAAFLTALILVNLKCGQRSKFGINRDA-VLAP 461
Qy      474 DDGASPLHHISNGSNTPSSSEGGPDAVITIGMTKIPVLENPOYRGITNSQLKPTTFQHI 533

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Db      462 EDGLAMSLHFWTLGGSSLSPTBGKSGSL-----QGHIMENPOYFS-----DTCVHHI 508
Qy      534 KRHNIVLKRRLGAGAGKVFALACYNLCPEQDKILVAVKTLKQASDNARQDFRREALLT 593
Db      509 KRQDILIKMELIGGAGKVFALACYNLQNDQMLVAVKLAKETSBARQDFRREALLT 568
Qy      594 NLQHEHLYKFGVCVGGDPLIMVFEEYMKHGDLLKPLRAHGPDAVILMAEGN--PPTBLTQS 651
Db      569 MLQHQHLYKFGVCVGGDPLIMVFEEYMKHGDLLKPLRAHGPDAVILMAEGN--PPTBLTQS 628
Qy      652 QMLHIAQILAGNYYLASQHFVARDLATRNCLVGENMLVKGDFGMSRDVYSTDYRVGG 711
Db      629 QLLAVASQVAAAGNYYLASLHFVARDLATRNCLVGGGLVYVIGDFGMSRDVYSTDYRVGG 688
Qy      712 HTMLPIRMPPESIMRKTTSSDVSLSGLVLMETFTYGKQPMYQLSNNEVEICTGGRV 771
Db      689 RTMLPIRMPPESIMRKTTSSDVSLSGLVLMETFTYGKQPMYQLSNNEVEICTGGRS 748
Qy      772 LORPTCPQEVYELMGCMQREPHMKIKIHLLQNLAKASPVYLDILG 822
Db      749 LERRPACPDVYALIMGCMQREPHMKIKIHLLQNLAKASPVYLDILG 799

```

RESULT 6

```

PCT-US04-30360-81
; Sequence 81, Application PC/TUS0430360
; GENERAL INFORMATION:
; APPLICANT: PLEXIKON, INC.
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
; FILE REFERENCE: 039363-1703
; CURRENT APPLICATION NUMBER: PCT/US04/30360
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/503,277
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 81
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Unknown Organism
; ORGANISM: INFORMATION:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian
; OTHER INFORMATION: protein sequence
PCT-US04-30360-81

```

Query Match 28.6%; Score 1263.5; DB 1; Length 337;

Best Local Similarity 68.6%; Pred. No. 1,26-69; Matches 240; Conservative 37; Mismatches 58; Indels 15; Gaps 3;

```

Qy      475 DQSAAPLHHISNGSNTPSSSEGGPDAVITIGMTKIPVLENPOYRGITNSQLKPTTFQHI 534
Db      1 DGLAMSLHFWTLGGSSLSPTBGKSGSL-----QGHIMENPOYFS-----DACVHHI 47
Qy      535 RHNIYVLRKELGEGAFGVFLAECYNLCPEQDKILVAVKTLKQASDNARQDFRREALLT 594
Db      48 RQIVLKRLELGBAFGVFLAECYNLCPEQDKILVAVKTLKQASDNARQDFRREALLT 107
Qy      595 LQHEHLYKFGVCVGGDPLIMVFEEYMKHGDLLKPLRAHGPDAVILMAEGN--PPTBLTQS 652
Db      108 LQHQHLYKFGVCVGGDPLIMVFEEYMKHGDLLKPLRAHGPDAVILMAEGN--PPTBLTQS 167
Qy      653 MLHIAQILAGNYYLASQHFVARDLATRNCLVGENMLVKGDFGMSRDVYSTDYRVGG 712
Db      168 LLAVASQVAAAGNYYLASLHFVARDLATRNCLVGGGLVYVIGDFGMSRDVYSTDYRVGG 227
Qy      713 TMPIRMPPESIMRKTTSSDVSLSGLVLMETFTYGKQPMYQLSNNEVEICTGGRV 772
Db      228 TMPIRMPPESIMRKTTSSDVSLSGLVLMETFTYGKQPMYQLSNNEVEICTGGREL 287
Qy      773 QRPPTCPQEVYELMGCMQREPHMKIKIHLLQNLAKASPVYLDILG 822
Db      288 LERRPACPDVYALIMGCMQREPHMKIKIHLLQNLAKASPVYLDILG 337

```


RESULT 7
US-10-450-763-50636
; Sequence 50636, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 50636
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (267)..(315)
; OTHER INFORMATION: Receptor tyrosine kinase class II proteins domain identified
; OTHER INFORMATION: by EMATRIX, accession number BL00239B, p-value=1.000e-40, raw scc
; OTHER INFORMATION: of 25.15
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (217)..(490)
; OTHER INFORMATION: Eukaryotic protein kinase domain identified by Pfam,
; OTHER INFORMATION: accession name pkinase, E-value=9.6e-96, Pfam score of 331.5
US-10-450-763-50636

Query Match 28.3%; Score 1249; DB 6; Length 503;
Best Local Similarity 73.7%; Pred. No. 1.4e-68;
Matches 232; Conservative 30; Mismatches 43; Indels 10; Gaps 2;

QY 510 VIENPOFGITNSQLKPDTPFOHAKRHNIYVKRELGEAFKGVLAECYNI.CPEODKTLV 569
DB 197 IIEPQYFS-----DACVHIKRDIVLKMELGEGAFKGVLAECYNI.LPDDKTLV 248
QY 570 AVKTLKASDVARQDFREAEELTNLOHEHIVKFGYCVESGDPLIMVPEYKHGDLNKL 629
DB 249 AVKTLKASDVARQDFREAEELTNLOHEHIVKFGYCVESGDPLIMVPEYKHGDLNKL 308
QY 630 RAHGPDAVLNABGN--PETELTOSQMLHIAQOIAAGWVYLAHQFVHRDLATRNCLVGEN 687
DB 309 RSHGPDAKLAGSDVAPGPIGLQLLAVASQVAAWVYLAHQFVHRDLATRNCLVGEN 368
QY 688 LLVKIGDFGMSRDVYSTDYRVGGHTMLPIRMMPESPIMYKFTTESDWSLGVLMEIF 747
DB 369 LLVKIGDFGMSRDVYSTDYRVGGHTMLPIRMMPESPIMYKFTTESDWSLGVLMEIF 428
QY 748 TYGQPMYQLSNNNVEICITOGVLAORPTQOEYVELMGCNREPIMRNKIGIHILL 807
DB 429 TYGQPMYQLSNNNVEICITOGVLAORPTQOEYVELMGCNREPIMRNKIGIHILL 488
QY 808 QNLAKASPVYLDILG 822
DB 489 QALAAAPVYLDVVG 503
RESULT 8
PCT-US04-23166A-729
; Sequence 729, Application PC/TUS0423166A
; GENERAL INFORMATION:
; APPLICANT: Purdue Pharma L.P.
; APPLICANT: Jiefel Tong
; APPLICANT: Gang Jin
; APPLICANT: Rui-Ru Ji
; APPLICANT: Yixun Xu

; APPLICANT: Lillian W. Chiang
; APPLICANT: Daniel J. Lavery
; TITLE OF INVENTION: GENES ASSOCIATED WITH RESPONSES TO NEUROPATHIC PAIN
; FILE REFERENCE: 02755/200M584-M00
; CURRENT APPLICATION NUMBER: PCT/US04/23166A
; CURRENT FILING DATE: 2004-07-06
; PRIOR APPLICATION NUMBER: 60/485,101
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 868
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 729
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US04-23166A-729

Query Match 17.3%; Score 763.5; DB 1; Length 502;
Best Local Similarity 37.2%; Pred. No. 3.6e-39;
Matches 183; Conservative 75; Mismatches 167; Indels 67; Gaps 15;

QY 10 PAMARLW-----GPCWL-VVGFMAAFACPTSCCKSARICSDPSGIYFPLRLP--- 60
DB 7 PAKCSFWRIFLLGSVWLDVVG--SVLACPANCVCSKTEICRRPDDGNL-FPLLEGDS 62
QY 61 -----NSVD-PENITTEIFIANOKRLBIINEDVEAYVGLRNLITVDSGLRFVAKA 110
DB 63 GNSGMSASINITDSRNTSIHIENMGGLHTLNAVDMELTYGLQKLTIKNSGLANIQPRA 122
QY 111 FLKNSNIQHINFTNKLTLSSRKHFRLDSELILVGNPFTGCDIMWIKTLQF-ANSSP 169
DB 123 FAKNPHLRVYNLSNRLTTLSSWQFLQTLRLRELLEQNFNCSDIRMMQLMOEGEARL 182
QY 170 DTQDLVCLNENSKNIPLANIQIPNCGP.SANLAPNLTVEGSKSITISCSVAGDPVPMY 229
DB 183 DSQSLYCLISADGSQLPFRNMISQCDLPEISVSHVNLTVEGDAVLTVCNCGSPLPVD 242
QY 230 MDVGNLVS-----KMMESHTOGSLRITNISDSDSGKQISCVANLVGSDVNLTVH 284
DB 243 WIVYGLQSINTHQTNLMTVTHAINLTLVNTSDENGFTLCLIMNVGMSNASVALITY 302
QY 285 PAPTITLESPTSDHMCIDPTVYKGNPKPALQWFFNGAIIINESKYICTKIHVNTTEYH- 343
DB 303 YPRVIVSLVPEVLEBICIEFVVGNGPPTLHMLYNGOPLRESKII-----HMDYYQ 354
QY 344 -----CCLQNDNPTNANGDYTLIAQBYGKDEKQISAPFMGPGIDDGANPYDVIY 397
DB 355 EGEVSEGCLEFKKETHNNGNYTLIAQNALGTANQTINGHFLKEP-----FPR--- 402
QY 398 EDVGTANDIGDTNRENEIPSTOVTDKGTREHLSYAVVAVVAVGFC-LVWMLPLL-- 454
DB 403 -----STDFDESASPTPTVTYHKPEBDYFGSIANGLAFA--CVLLVVLFTMIN 454
QY 455 KLAHRSKFGMG 466
DB 455 KYGRBSKFGMG 466
RESULT 9
PCT-US04-30360-82
; Sequence 82, Application PC/TUS0430360
; GENERAL INFORMATION:
; APPLICANT: PLEXIXON, INC.
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
; FILE REFERENCE: 039363-1703
; CURRENT APPLICATION NUMBER: PCT/US04/30360
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/503,277
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 82
; LENGTH: 345
; TYPE: PRT

Query Match 15.4%; Score 679.5; DB 6; Length 1367;

Best Local Similarity 25.7%; Pred. No. 1.4e-33;
Matches 242; Conservative 128; Mismatches 279; Indels 293; Gaps 41;

```
QY 93 LRNLTIYDSGLKFAVHAKAF--LKNSNLQHI--NFTRNKLTSLSRKH-----RHLDSEIL 145
D 402 LKNRLILGEGQLGNGNSFYVLDNQLQMDMDHRLNLTIRAGKMYFAFNPKLCVSELYR 461
QY 146 V-----GNPFTSCDIMWIKTLQEAKS-----SPDTODLY 175
D 462 MEEVYTGKRGSKGDINTRNNGERASCESDVLHFTSTTSKRIITWHRYPDPYDLI 521
QY 176 CLNSSFNPIPLANOIR-----CGLPSANLA-----APRLTYEBG----- 211
D 522 SFVYVYKAPPKVNTYDGDACGNSNMWVDVLPPKQDVEPGILLHGLKPMTOYAVYV 581
QY 212 KSITLSCSVAGD-----PVENMTWV-----GN 234
D 582 KAVVLT--MVENDHIRGAKSELITRTNASTVPSIFLVDLSAENSSQILVKNPSPLRNGN 640
QY 235 L-----VSKHNETS-----HTQSLRI-----TNISDDSGQ 263
D 641 LSYIVVWQROPQDGYLYRH--NYCSKDKIPIRKYADGTIDIEVTENPKTEVCGEKGPC 699
QY 264 ISC-----VAENLVGEDDSVNLTYH--FAP-----TTFLESPTSDDHM 301
D 700 CACPKTEAKQAEKEAEYRKYFENFLNLSIFVRPERKRDVNOVANVTSSRSRNTYA 759
QY 302 CIPFTVGNPKPALOW--FYNGAILNESKYICTK-----IHTVNH--TEHYGCLQD 349
D 760 ADYVNIIDPELETFEYFPFESRVDNKERTVLSNRPFTLYRIDHSCHEAEKLGCC--- 815
QY 350 NPTMNGDYLTLAKNEYGDE-----KOISAHFMGWPGLDGANPNYPVIVE-D 399
D 816 ---SASFVFAITMPAE--GADDIPGVTWEPRENSIFLKP---EPENNGILLMTEIK 868
QY 400 YGTAANDI-----GDTTRNSN-----EIPSTDV-----TD-----KT 426
D 869 YGSOVEQRECVSHQERYKYGAKLNRLNPGNYTARIQATSLSGNSWTDVFFVYQAKT 928
QY 427 GRE---HLASYAVVAVIASVVGFCLLVMLFLKLARHSGFKGKGPASVYSNDDASPLHH 483
D 929 GYEFHILIALPVALVILV--GLVIMLV-----FHR 960
QY 484 ISNGSNTSSSEGGPDVAIIGMTKIPVLENPOYFGITNSQLPPTFYOHIKSHNIYAKRE 543
D 961 KRNNR-----LGNGVLYASVNPETFSADVYV--PDEM--EVARREKITMSRE 1004
QY 544 LGEGAFKVLAECCYNLCPEQDKILVAVKTLKQ--ASDNARKDFRREALLTNLOHEHIVK 602
D 1005 LGQSGFQVYVEGAVKGVKDEPETRVAIKTYNEAASMRERLEFLNEASVMKEFNGCHVVR 1064
QY 603 FYGCVGEGDPLIMVFEYMKHGDILNKLRAHGPDAVLAEGNP---PTELLOSQMLHAQ 659
D 1065 LLAGVSGOQPLTVIMELTRDILKSYLSRLE---MENNPVALAPPSL--SKMIOVAGE 1118
QY 660 IAAGMVYASQHFYHRLDTRNCLVGENLVKIGDPMGSRDVSITDYRYGVGHMLPRLW 719
D 1119 IADGMATLANKFHRDLAARNCVAEDFTYKIGDPMGTRDIYETDYIRKGGKGLLPFRW 1178
QY 720 MPBSIMYRKTTESDVWSLGVLMELFTYKQPMYOLSNNEVEICTOGFVLORPRTCP 779
D 1179 MSPBSLADGVFTTYSVWSPGVVLMELATLAEPYQGLSNGQVAFPMWEGGLDKPNDP 1238
QY 780 QEVVELMGLCQRPFRHAKNIKGIIHTLQNLAKASPVYLDL 821
D 1239 DMLEFELMRMCQYNPKOR-----PSFLEII 1263
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RESULT 12
PCT-US04-42360-862
; Sequence 862; Application PC/TUS0442360
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General

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; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: 17633/2048
; CURRENT APPLICATION NUMBER: PCT/US04/42360
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: 60/531,341
; NUMBER OF SEQ ID NOS: 2587
; SOFTWARE: perl script
; SEQ ID NO 862
; LENGTH: 1370
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Refseq / NP_434694
; DATABASE ENTRY DATE: 2003-10-05
PCT-US04-42360-862
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Query Match 15.3%; Score 676; DB 1; Length 1370;

Best Local Similarity 24.4%; Pred. No. 2.3e-33;
Matches 258; Conservative 134; Mismatches 300; Indels 366; Gaps 45;

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QY 32 CPTSCKSASR-----IWCSDPSRGIYAFRLERNSVDPENITEL-----FINOK 77
D 307 CPGSGFIRNSTQSMYCIPECBPCPCVCGDEBKTKTIDTSVSAQMLQCTTLKGNLLINIR 366
QY 78 RLRIINEDVYEAAYG-----LRNLTIYDSGLKFAVHAKAF--LK 113
D 367 RGNNT--ASELENFGLIEVYTGKYNHSHALVSLSLKILRLILGEGQLGNGNSFYVLD 425
QY 114 NSNLQHI--NFTRNKLTSLSRKH-----RHLDSEILV-----GN 148
D 426 NQNLQQLMDMNHRLNLTYSRGOMYFAFNPKLCVSEIYMEVYTGKRGSKGDINTRNNGE 485
QY 149 PFTSCDIMWIKTLQEAKS-----SPDTODLYCLNSSFNPIPLANOIR-----C 194
D 486 RASCESDVLFTSTTKNRIITWHRYPDPYDLISFVYVYKAPPKVNTYDGDQAC 545
QY 195 GLPSANLA-----APNLVBERG-----KSITLSCSVAGD----- 223
D 546 GSNMNMWVDVLPPNKEGEGILLHGLKPMTOYAVVYKAVVLT--MVENDHIRGAKSELTY 604
QY 224 ---PVNMYWV-----GNL-----VSKHNE 242
D 605 IRTNASTVPSIFLVDLSAENSSQILVKNPPTLPNGLSYIYRWQROPQDGYLYRH--NY 663
QY 243 TS-----HTQSLRI-----TNISDDSGKQISC-----VA 268
D 664 CSKDKIPIRKYADGTIDIEVTENPKTEVCGDPCACPKTEAKQAEKEAEYRKFV 723
QY 269 ENLVGED-----QDSVNL--VHFAPITTFLESPT 296
D 724 ENFLHNSIFVPRPERRRRDVLQVANVTSSRSRNTVAADVTNITDPEEFETEPFESRV 783
QY 297 SDHMCIPFTVGNPKPALQWPFYNGAILNESKYICTKIHTVNH--TEHYGCLQDNPHTMN 355
D 784 DNE-----RVIISNLRFTYLRID-----IHCNHEAEKLGCC-----SAS 819
QY 356 NGDYTLIAKNEYGDE-----KOISAHFMGWPGLDGANPNYPVIVE--DYGTAA 405
D 820 NFVFAITMPAE--GADDIPGVTWEPRENSIFLKP---EPENNGILLMTEIKYGSOVE 875
QY 406 DI-----GDTTRNSN-----EIPSTDV-----TD-----KTGRE--- 429
D 876 DQRECVSROERYKYGAKLNRLNPGNYTARIQATSLSGNSWTDVPPFVYPAKTYNFM 935
QY 430 HLSYAVVAVIASVVGFCLLVMLFLKLARHSGFKGKGPASVYSNDDASAPLHHISGNS 489
D 936 HLIILPVALVILV--GLVIMLV-----FHRKRNNR 967
QY 490 TPSSSEGGPDVAIIGMTKIPVLENPOYFGITNSQLKEDTFVQHIKRNIYAKRELGCAF 549
D 968 -----LGNGVLYASVNPETFSADVYV--PDEM--EVARREKITMNRLELGQSGF 1011
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QY 550 GKFLAECYNLCPEBQKILVAVTKLKD-ASDNARKDFHRAEELLTNLOHEHIYKPYGCV 608
 Db 1012 GMVYEGVAKGVNDDEPRTVAIKVMEASMRERIEFLNBSYKKEFNCHVRLGVS 1071
 QY 609 EGDPLIMVFPMYKHKDNTKILRAHGPDAVMAEGN-----PPTTELQSOMLHIAQOIAAGM 664
 Db 1072 QGGPTVLIMELMRGDKLSTLRSPR-----VENNLVLTP-----SLSKMLQMGAGELADGM 1124
 QY 665 VYLAQHVFHARDLATRNCVLGENMLVKIGDFGMSRDVYSTDYRVGHTMLPIRMMPES 724
 Db 1125 AYLNANKFVARHDLAARCMVAABDPTVKIGDFGMRDRIYEDDYRKGGKGLLPIRMMPES 1184
 QY 725 IMRKFTTESDWSLGVLMELIFTYGQPMYOLSNNEVICITQGRVLOPRCPQEVYZ 784
 Db 1185 LKQGVFTTHSDVMSFGVLMELIATLAEQPYQGLSNEGVLFVMEGGLDPRDNCDDMLFE 1244
 QY 785 LMLGCMQREPMHNRKINIGHTLLQNLAKASPVYLDIG 822
 Db 1245 LMRMCWQYFPRMR-----PSFLEIIG 1265

RESULT 13

PCT-US04-30360-83
 ; Sequence 83, Application PC/TUS0430360
 ; GENERAL INFORMATION:
 ; APPLICANT: PLEXIKON, INC.
 ; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
 ; FILE REFERENCE: 039363-1703
 ; CURRENT APPLICATION NUMBER: PCT/US04/30360
 ; CURRENT FILING DATE: 2004-09-15
 ; PRIOR APPLICATION NUMBER: 60/503,277
 ; PRIOR FILING DATE: 2003-09-15
 ; NUMBER OF SEQ ID NOS: 167
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 83
 ; LENGTH: 376
 ; TYPE: PRT
 ; ORGANISM: Unknown Organism
 ; FEATURE:
 ; OTHER INFORMATION: Description of Unknown Organism: Mammalian
 ; OTHER INFORMATION: protein sequence
 PCT-US04-30360-83

Query Match 14.9%; Score 660; DB 1; Length 376;
 Best Local Similarity 43.5%; Pred. No. 4.8e-33;
 Matches 136; Conservative 51; Mismatches 112; Indels 14; Gaps 5;

QY 509 PVLENPQYFGITNSQL-----KPDTFVQHKIKRNIYVKRELGGAGKVPFLAECYNLCR 562
 Db 16 PVOROPFGHVGONVEMMLNAYKKSXAKELPLSAVFPMELGRCARFGKTYKGLY--LP 73
 QY 563 EODKI-LVAAYKTLKDAASDNAR-KDFHREAEELLTNLOHEHIYKFGVCEBGDPLIMVPEYM 620
 Db 74 GMDHAQVLAIKTLVDYNNPQOMMEFOQBASIMAEHLHPNIVCLIGAVTQROPVCMLEBYI 133
 QY 621 KHGDLNKLRAHGPDAVMA-----EGNPTELTQSOMLHIAQOIAAGVYLAHQHVFYARD 676
 Db 134 NQGDHLHFLMRSHSDVGCSSDSDGTVKSLSHDGDLHLIAIQAAAMEYLSHFFVHKD 193
 QY 677 LATRNCVLGENMLVKIGDFGMSRDVYSTDYRVGHTMLPIRMMPESIMRKFTTESDV 724
 Db 194 LAARNILIGELQHLKIDLGISREIYADYRVQSKSLPIRMMPRAIMYGKSSDSDI 253
 QY 737 MSLGVLVMEIFTYQKQPMYOLSNNEVICITQGRVLOPRCPQEVYELMLGCMQREPMH 796
 Db 254 MSFGVLMELIFSGLOPYGFSNQGVILMWAKRQLLPCSDCPRPMYSLMTECWNELPSR 313
 QY 797 RKNKIGITLLON 809
 Db 314 RPRFKDHLVRLRS 326

RESULT 14

PCT-US05-00638-81
 ; Sequence 81, Application PC/TUS0500638
 ; GENERAL INFORMATION:
 ; APPLICANT: Clark, Edwin
 ; APPLICANT: Clark, Edwin
 ; APPLICANT: Jordan, Shirlin
 ; APPLICANT: Yoganathan, Suganthy
 ; TITLE OF INVENTION: BIOMARKERS AND METHODS FOR DETERMINING SENSITIVITY TO EPIDERMAL
 ; GROWTH FACTOR RECEPTOR MODULATORS
 ; FILE REFERENCE: 10159 PCT
 ; CURRENT APPLICATION NUMBER: PCT/US05/00638
 ; CURRENT FILING DATE: 2005-01-07
 ; PRIOR APPLICATION NUMBER: US 60/535,151
 ; PRIOR FILING DATE: 2004-01-07
 ; NUMBER OF SEQ ID NOS: 125
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 81
 ; LENGTH: 806
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 PCT-US05-00638-81

Query Match 14.8%; Score 654; DB 1; Length 806;
 Best Local Similarity 26.6%; Pred. No. 2.7e-32;
 Matches 204; Conservative 122; Mismatches 267; Indels 174; Gaps 29;

QY 141 SELILGNPPTGSCDLMWIKTLQEAQSSPDYDLYCLINSSKNIPYANLQIPNCGLPISA- 199
 Db 84 SEVVLVGP-----QRLQVLAHSHEDSAGYCRQLRLTRVLCHEFSVRVTADPSSG 132
 QY 200 -----NLAPN-----LTVEGSKITLSCSYAGDPVPMYV----- 230
 Db 133 DDEGDEADBDTGVDCGAPYWTFRPERMDKLLAVPAANTYFRCPAAGNTPSISMLKNG 192
 QY 231 -----DVCNLYSKMNETSHQGLRITNISDSDGKQISGVANLVGEDDSDVNLTV 283
 Db 193 REFRGHRIGGI-----KLRHQWLSLWESVPSDRG--NYTCVENKFGSIRQTYTLDV 245
 QY 284 -HEAPITTFLESPTSDHNMCI-----PFTVGNPKPALQWYFNGALINSEK----- 328
 Db 246 LERSPHRPIQALPANCQRAVLGSDVEFHCKYVSDAQPHIQMLKHYEV--NGSKVGPDGP 304
 QY 329 YICT-KIHVTNTEYH-GCLQDNPTHMNGDYTLIAKNEYGDEKQISAHFMGPGIDD 386
 Db 305 YVTVLKTAGANTTDKELEVLSLHNVTFEDAGEYTCLAGNSIG-----FSHSHAMLVV-- 356
 QY 387 GANPNYVDVYEDYGTANDIGDTTRNSNEIPSTD---VTDKTGREHLSYAAVYVLAIVV 443
 Db 357 -----LPRAEELVEADEAG---SVYAGILSYGVG 382
 QY 444 GFCLVWLFLKLAR-----H--SKFGMKGPASYISNDDDSASPLHHISNG 487
 Db 383 FFLFELIVAAVTLCTRLSPKKGSLGSPYHKIRFLPKQVLSLSN-----ASMS 432
 QY 488 SNTSSSBGGPDVILIGMTKIPVLENPQYFGITNSQLKPDTFVQHKIKRNIYVKRELGG 547
 Db 433 SNTP-----LVRIATLSGEGPTLANVELLELPADP--KWEISRARLTGKPGEG 481
 QY 548 AFGKVLAECCYNLCPEBQK-----LVAAYKTLK-DASDNARKDFHRAEELLTNLOHEHIY 601
 Db 482 CFQGVMAEAIIGI--DKDRAKPVYAAVKNLKDADADKDLSDVSEEMMKMGKHNII 539
 QY 602 KFYGVCEBGDPLIMVPEYMGGLNKLFLRAHGPDAV--LMAEGNPTE-LTQSOMLHIAQ 658
 Db 540 NLIGACTQGGPVLVLYEYAAKGNLREFLRARRRPGLDYSDTCKPFEQGLTFKDIYSCAY 539
 QY 659 QIAAGVYLAHQHVFHARDLATRNCVLGENMLVKIGDFGMSRDVYSTDYRVGHTMLPIR 718
 Db 600 QVARGMETLASQKCHRDILAAARVVLVEDVNMKIDAGGLARDVHNLDYKKTNGRLPVK 659
 QY 719 WMPDESIMRKFTTESDWSLGVLMELIFTYGQPMYOLSNNEVICITQGRVLOPRPTC 778

Db 660 WMAPEALFDRVYTHQSDVWSFGVLLMEIFTLGSSPYEGIPVEBELFKLIKEGRMDKQANC 719
QY 779 POEVEELMGCMQREPHMRKNKIGIHITLLQNLAKASPV-----YLDI 820
Db 720 THDLYMIMRECBMHAAPSGRPTEK---QVDEDDLVLTSTSTDEYIDL 763

RESULT 15
PCT-US04-30360-50
Sequence 50, Application PC/TUS0430360
GENERAL INFORMATION:
APPLICANT: PLEXIKON, INC.
TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
FILE REFERENCE: 039363-1703
CURRENT APPLICATION NUMBER: PCT/US04/30360
CURRENT FILING DATE: 2004-09-15
PRIOR APPLICATION NUMBER: 60/503,277
PRIOR FILING DATE: 2003-09-15
NUMBER OF SEQ ID NOS: 167
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 50
LENGTH: 370
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Mammalian
PCT-US04-30360-50

Query Match 14.3%; Score 634; DB 1; Length 370;
Best Local Similarity 43.4%; Pred. No. 1.8e-31;
Matches 131; Conservative 51; Mismatches 110; Indels 10; Gaps 5;

QY 513 NPOVFGITN----SQLKPDFTVGHKIKRHNITLKRLEGGAGKVFYLAECYTLCEPDKITL 568
Db 24 NPEYLSASDVFPCCSVYVPDEM--EVSREKLTLLRELGQSGFQWVYEGNARDIIRGEAETR 81
QY 569 VAVETLKD-ASDNARKDFHREAEELTNLQHEHIVKFGVCVEGDPLIMVPEYMGDLNK 627
Db 82 VAVTVNESASLRERIEFLNLSASVYKGTCHHVRLGLGVSKQPTLVVWELMAHGDLS 141
QY 628 FLAHGPDVYLMAGNPPTELTQSOMLHIAQOIAAGVYIASQHVRHDLATRNCLVGEN 687
Db 142 YLRSIRPEAB-NNPRPPP--TLQEMIQMAEIRADGMAVYLNAKKFFVRHDLAARCNVAHD 198
QY 688 LTVKIGSGMSRDVYSTDYVAVGHTMLPIRMPPESIMRKFTTESDWSLGVVLMEIF 747
Db 199 FTVKIGDPMTRDIYETDYRKGGKGLPVKMMAPESLKDGVFTTSSDMWSFGVVLWEIT 258
QY 748 TYGQPMYQLSNNEVICITQGRVLABRPTCPQEVVELMLGCMQREPHMRKNKIGIHITLL 807
Db 259 SLAEQPYQGLSNEGVLFKVMDDGVLDDPCNPERVTDLMRCMQPNPMRPTFLIYVNL 318
QY 808 QN 809
Db 319 KD 320

Search completed: February 17, 2005, 00:18:59
Job time : 29 secs

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Db 241 ACCGAGAGTTAAAGAGCCGCAAGCCGAGGAAAGCCTCCCCACGCGGGGAAAG 300
Qy 301 CGCGCGGTGACGCGCGGGGACAGGCACTCGGCTGAGACTGCTGTAAGGATGTCGTC 360
Db 301 CGCGCGGTGACGCGCGGGGACAGGCACTCGGCTGAGACTGCTGTAAGGATGTCGTC 360
Qy 361 TGGATTAAGTGGCATGGAACCCGCAATGGCGCTCTGGGGCTTCTGCTGGCTGGTGG 420
Db 361 TGGATTAAGTGGCATGGAACCCGCAATGGCGCTCTGGGGCTTCTGCTGGCTGGTGG 420
Qy 421 GGCCTTCTGAGGGGCGCTTTCGCTGCTCCAGCTCCGCAAAATGCAAGGCTCTCGGATC 480
Db 421 GGCCTTCTGAGGGGCGCTTTCGCTGCTCCAGCTCCGCAAAATGCAAGGCTCTCGGATC 480
Qy 481 TGGTGACGACGACCTTCTCTGAGCATGCTGAGCAATTCGAGATTGAGACCTTAACGTGA 540
Db 481 TGGTGACGACGACCTTCTCTGAGCATGCTGAGCAATTCGAGATTGAGACCTTAACGTGA 540
Qy 541 GATCTTGAGAACTATCAGCGAAATTTTCACTGCGAAACGAGAAAGTTAGAAATCATCAAC 600
Db 541 GATCTTGAGAACTATCAGCGAAATTTTCACTGCGAAACGAGAAAGTTAGAAATCATCAAC 600
Qy 601 GAAGATGATGTTGAAGCTTATGAGGACCTGAGAAATCGCAATTTGATGATTCGAGTTA 660
Db 601 GAAGATGATGTTGAAGCTTATGAGGACCTGAGAAATCGCAATTTGATGATTCGAGTTA 660
Qy 661 AAATTTGTGCTCATPAAAGATTCTGAAAAACAGCAACCTGACGACATCAATTTTACC 720
Db 661 AAATTTGTGCTCATPAAAGATTCTGAAAAACAGCAACCTGACGACATCAATTTTACC 720
Qy 721 CGAAAACAACTGACGAGTTGTCTAGAGAAATTCCTGTCACCTTGACTTGTCTGAACCTG 780
Db 721 CGAAAACAACTGACGAGTTGTCTAGAGAAATTCCTGTCACCTTGACTTGTCTGAACCTG 780
Qy 781 ATCTGAGGAGCAATTCATTTACATGCTCCTGTCACATTAATGAGGATCAAGACTCTCA 840
Db 781 ATCTGAGGAGCAATTCATTTACATGCTCCTGTCACATTAATGAGGATCAAGACTCTCA 840
Qy 841 GAGGCTAAATTCAGTCCAGACACTCAGGATTTGTACTGCTGATGAGGAGAGCAAGAT 900
Db 841 GAGGCTAAATTCAGTCCAGACACTCAGGATTTGTACTGCTGATGAGGAGAGCAAGAT 900
Qy 901 ATTCCCTGCGAAACCTGCGAGATACCCAAATTTGTGCTTCCATCTGCAAACTTGCCGCA 960
Db 901 ATTCCCTGCGAAACCTGCGAGATACCCAAATTTGTGCTTCCATCTGCAAACTTGCCGCA 960
Qy 961 CCTAACCTCACTGAGGAGAAAGTATCACTTATCTGTAGTGGCGAGGTAT 1020
Db 961 CCTAACCTCACTGAGGAGAAAGTATCACTTATCTGTAGTGGCGAGGTAT 1020
Qy 1021 CGGTTCTATATATGATTTGGATGTTGTAACTGTGTTTCAAAACATATGAATGAACA 1080
Db 1021 CGGTTCTATATATGATTTGGATGTTGTAACTGTGTTTCAAAACATATGAATGAACA 1080
Qy 1081 AGCCACACACAGGCTCTTAAGGATTACTTAACATTTCACTCGAGTCAAGTGGAGACAG 1140
Db 1081 AGCCACACACAGGCTCTTAAGGATTACTTAACATTTCACTCGAGTCAAGTGGAGACAG 1140
Qy 1141 ATCTCTGTGTGGGAGAAATCTTGTAGAGAGATCAAGATTTGTGCAACTTCACTGAGT 1200
Db 1141 ATCTCTGTGTGGGAGAAATCTTGTAGAGAGATCAAGATTTGTGCAACTTCACTGAGT 1200
Qy 1201 CATTTTGACCAATATACATTTCTGAAATCTCAACCTGACACCACTGATGTGATT 1260
Db 1201 CATTTTGACCAATATACATTTCTGAAATCTCAACCTGACACCACTGATGTGATT 1260
Qy 1261 CCATTAACCTGTGAAGGCAACCCCAACCAAGCGCTTCAGTGTGTTCTATTAACGGGGCAATA 1320
Db 1261 CCATTAACCTGTGAAGGCAACCCCAACCAAGCGCTTCAGTGTGTTCTATTAACGGGGCAATA 1320
Qy 1321 TTGAATGAGTCCAAATATCATCTGATCTAAATATATGTTACCAATCAAGGATACAC 1380
Db 1321 TTGAATGAGTCCAAATATCATCTGATCTAAATATATGTTACCAATCAAGGATACAC 1380

Db 1321 TTGAATGAGTCCAAATATCATCTGATCTAAATATATGTTACCAATCAAGGATACAC 1380
Qy 1381 GGCCTGCTCCAGCTGATTAATCCCACTACATGAAACATAGGGGACTACCTTAATAGCC 1440
Db 1381 GGCCTGCTCCAGCTGATTAATCCCACTACATGAAACATAGGGGACTACCTTAATAGCC 1440
Qy 1441 AAGATGATGATGAGAAAGATGAGAAACAGATTTCTGCTCATCTTATGAGGCTGGCTGGA 1500
Db 1441 AAGATGATGATGAGAAAGATGAGAAACAGATTTCTGCTCATCTTCAAGGCTGGCTGGA 1500
Qy 1501 ATTGACATGATGAGAAACCCCAATTAATCCATGATTAATTAATGAAGTTATGGAACCTGCA 1560
Db 1501 ATTGACATGATGAGAAACCCCAATTAATCCATGATTAATTAATGAAGTTATGGAACCTGCA 1560
Qy 1561 GCGAATGACATCGGGGACACACGAAACAGAGTAATGAAATCCCTTCCAGACGTCACCT 1620
Db 1561 GCGAATGACATCGGGGACACACGAAACAGAGTAATGAAATCCCTTCCAGACGTCACCT 1620
Qy 1621 GATPAAACCGGTGGGAAACTCTCTCGGTCTAATGCTGTGGTGGATTGCGTCTGTGGTG 1680
Db 1621 GATPAAACCGGTGGGAAACTCTCTCGGTCTAATGCTGTGGTGGATTGCGTCTGTGGTG 1680
Qy 1681 GGAATTTGCTTTGTTGTTATGCTGTTCTGCTTAAGTTGGCAAGACCTCAAGTTGGC 1740
Db 1681 GGAATTTGCTTTGTTGTTATGCTGTTCTGCTTAAGTTGGCAAGACCTCAAGTTGGC 1740
Qy 1741 ATGAAAGCCGACGCTCCGTTATCAGCAATGATGATGATCTGCGACGCCATCCATCAC 1800
Db 1741 ATGAAAGCCGACGCTCCGTTATCAGCAATGATGATGATCTGCGACGCCATCCATCAC 1800
Qy 1801 ATCTCCAAATGGAGTAACTCCATCTTCTGGAAGGTGGCCAGATGCTGTCAATTA 1860
Db 1801 ATCTCCAAATGGAGTAACTCCATCTTCTGGAAGGTGGCCAGATGCTGTCAATTA 1860
Qy 1861 GGAATGACAAAGATCCCTGTCATTTGAAATCCCAAGTACTTGGCATCAACACAGTCAG 1920
Db 1861 GGAATGACAAAGATCCCTGTCATTTGAAATCCCAAGTACTTGGCATCAACACAGTCAG 1920
Qy 1921 CTCAGGCAAGACATTTGTTGAGCACTCAACGACATTAATGTTCTGAAAAGGAG 1980
Db 1921 CTCAGGCAAGACATTTGTTGAGCACTCAACGACATTAATGTTCTGAAAAGGAG 1980
Qy 1981 CTAGGCGAAGAGCCTTTGAAAAGTGTCTTAGCTGAATGCTAATACTCTGTCTGAG 2040
Db 1981 CTAGGCGAAGAGCCTTTGAAAAGTGTCTTAGCTGAATGCTAATACTCTGTCTGAG 2040
Qy 2041 CAGGACAAAGTCTTGGGAGAGGAGACCTGAAGGATGCGATGCAATGACAGCAG 2100
Db 2041 CAGGACAAAGTCTTGGGAGAGGAGACCTGAAGGATGCGATGCAATGACAGCAG 2100
Qy 2101 GACTTCCACCGTAGAGGCGAGCTCTGACCAACCTCCAGATGAGCACTGTCAAAGTT 2160
Db 2101 GACTTCCACCGTAGAGGCGAGCTCTGACCAACCTCCAGATGAGCACTGTCAAAGTT 2160
Qy 2161 TATGGGCTGTGCTGAGAGGCGACCCCTCATATGATCTTTGAGTACATGAAGCATGG 2220
Db 2161 TATGGGCTGTGCTGAGAGGCGACCCCTCATATGATCTTTGAGTACATGAAGCATGG 2220
Qy 2221 GACTCAACAAAGTTCCTCAAGGAGCAACGAGCCCTGAAGGCGGTGATGAGTGGAGGCAAC 2280
Db 2221 GACTCAACAAAGTTCCTCAAGGAGCAACGAGCCCTGAAGGCGGTGATGAGTGGAGGCAAC 2280
Qy 2281 CGGCGCACGGAATGACGAGTGCAGATCTCATTTAGCCAGCAGATGCGCGCGGGC 2340
Db 2281 CGGCGCACGGAATGACGAGTGCAGATCTCATTTAGCCAGCAGATGCGCGCGGGC 2340
Qy 2341 ATGATCTACCTGCGCTGCCAGCACTTGTGACCCGGAATTTGGCCACAGAACTGCTG 2400
Db 2341 ATGATCTACCTGCGCTGCCAGCACTTGTGACCCGGAATTTGGCCACAGAACTGCTG 2400
Qy 2401 GTGCGGAGAACTTGTGCTGTGAAATCCGGGAACTTTGGATGTGCCGGAGCGTGTACAGC 2460
Db 2401 GTGCGGAGAACTTGTGCTGTGAAATCCGGGAACTTTGGATGTGCCGGAGCGTGTACAGC 2460

QY 2461 ACTGACTCTACAGGGGTGGTGGCCACAAATGCTGCCATTCGCTGGATGCTTCGAG 2520
 DB 2461 ACTGACTCTACAGGGGTGGTGGCCACAAATGCTGCCATTCGCTGGATGCTTCGAG 2520
 QY 2521 AGCATGATGACAGAAATTCAGACGGGAAGCGATGCTGAGCCTGGGGGTGTGTG 2580
 DB 2521 AGCATGATGACAGAAATTCAGACGGGAAGCGATGCTGAGCCTGGGGGTGTGTG 2580
 QY 2581 TGGGAGATTTTCACTTATGAGCAACAGCCCTGTACACGCTGTCAAAATGAGTGATA 2640
 DB 2581 TGGGAGATTTTCACTTATGAGCAACAGCCCTGTACACGCTGTCAAAATGAGTGATA 2640
 QY 2641 GAGTGATCACTCAGGGCCGAGTCTTGACGGACCCCGACGTCGCCCCAGAGGTGTAT 2700
 DB 2641 GAGTGATCACTCAGGGCCGAGTCTTGACGGACCCCGACGTCGCCCCAGAGGTGTAT 2700
 QY 2701 GAGTGATGCTGGGGGTGTGGCAGCAGAGGCCCAATGAGGAAGAAATTAAGGATC 2760
 DB 2701 GAGTGATGCTGGGGGTGTGGCAGCAGAGGCCCAATGAGGAAGAAATTAAGGATC 2760
 QY 2761 CATACCTCTCTGAGAACTTGGCCAGGCAATCTCCGCTTACCTGAGACATTTAGGCTAG 2820
 DB 2761 CATACCTCTCTGAGAACTTGGCCAGGCAATCTCCGCTTACCTGAGACATTTAGGCTAG 2820
 QY 2821 GGGCCCTTTCCCGACAGCCGATCTTCCCAAGTACTCTCAGACGGGCTGAGAGATGAA 2880
 DB 2821 GGGCCCTTTCCCGACAGCCGATCTTCCCAAGTACTCTCAGACGGGCTGAGAGATGAA 2880
 QY 2881 CATCTTTTAACTGCGCGCTGAGAGCCACCAAGCTGCTCTTCACTCTGACGATTTAC 2940
 DB 2881 CATCTTTTAACTGCGCGCTGAGAGCCACCAAGCTGCTCTTCACTCTGACGATTTAC 2940
 QY 2941 ATCAAAGCTCCGAGAGCTCTGAGGGGAAGCAGTGTATCTTCACTCATAGACACA 3000
 DB 2941 ATCAAAGCTCCGAGAGCTCTGAGGGGAAGCAGTGTATCTTCACTCATAGACACA 3000
 QY 3001 GTATGACCTCTTTTGGCATTAATCTCTTCTCTTCCATCTCCCTGGTGTCTCTT 3060
 DB 3001 GTATGACCTCTTTTGGCATTAATCTCTTCTCTTCCATCTCCCTGGTGTCTCTT 3060
 QY 3061 TTTCTTTTAAATTTTCTTTTCTTTTCTTTTCTGCTCCCTGCTCAGATTTCTT 3120
 DB 3061 TTTCTTTTAAATTTTCTTTTCTTTTCTTTTCTGCTCCCTGCTCAGATTTCTT 3120
 QY 3121 ACCCTTCTTTGATCAATCTGCTCTGATTAATACTGATGACAAAGGC 3180
 DB 3121 ACCCTTCTTTGATCAATCTGCTCTGATTAATACTGATGACAAAGGC 3180
 QY 3181 CTTTAAACAGTATTTGTATATCAGACAGACCTCCAGTTTGGCCACCACTAACAA 3240
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 REFERENCE 1 (bases 1 to 3707)
 Nakagawara, A., Liu, X. G., Ikegaki, N., White, P. S., Yamashiro, D. J., Nycum, L. M., Biegel, J. A. and Brodeur, G. M., Cloning and chromosomal localization of the human TRK-B tyrosine kinase receptor gene (NTRK2) Genomics 25 (2), 538-546 (1995)
 JOURNAL MEDLINE 95309922
 PUBMED 7789988
 REFERENCE 2 (bases 1 to 3707)
 Nakagawara, A., Submitted
 Direct Submission
 Submitted (08-JUL-1994) Akira Nakagawara, Division of Oncology, Children's Hospital of Philadelphia, 34th & Civic Center Blvd., Philadelphia, PA 19104, USA
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REFERENCE
1 (bases 1 to 4057)
Stojlov P., Castren, B. and Stamm, S.
Analysis of the human TrkB gene genomic organization reveals novel
TrkB isoforms, unusual gene length, and splicing mechanism
Biochem. Biophys. Res. Commun. 290 (3), 1054-1065 (2002)
JOURNAL MEDLINE
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REFERENCE 2 (bases 1 to 4057)
Stojlov P.G., Castren, B. and Stamm, S.
Direct Submission
Submitted (16-AUG-2001) Institute of Biochemistry, FAU Erlangen,
Faculty of Medicine, Fahrstrasse 17, Erlangen 91054, Germany
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LOCUS Sequence 1 from patent US 5844092.
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ACCESSION AR063152

VERSION AR063152.1 GI:5990843
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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 3194)
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JOURNAL Human TRK receptors and neurotrophic factor inhibitors
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 SOURCE
 ORGANISM
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 Unclassified.
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 AUTHORS Presta,L.G., Shelton,D.J., and Ufer,R.
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Db	3074	ACTTCTGCTGTACAGATATCGAGAGTTCTATGATTAACCTTCTAATTATTAATTAATAT	3133
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Db	3134	TACTGTTCTTAATGTTTTTGGATGGCTTAACCTGTGTATTAATAAAGAAA	3184

[illegible]

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Db	554	CAATCCATTTACATGCTCTGTGACATTTATGTGATCAAGACTCTCCAAAGGCTAAATC	613
QY	852	CAGTCCAGACACTGAGAGTTTGTACTGCTGCAATGAAGACGACAAAGATATTTCCCTGGC	911
Db	614	CAGTCCAGACACTGAGAGTTTGTACTGCTGCAATGAAGACGACAAAGATATTTCCCTGGC	673
QY	912	AAACCTGACAGTACCACAAATTTGGTTGGCCATCTGCAAAATCTGGCCGCACTTAACCTCAC	971
Db	674	AAACCTGACAGTACCACAAATTTGGTTGGCCATCTGCAAAATCTGGCCGCACTTAACCTCAC	733
QY	972	TGTGAGAGAAAGAAAGTCTATCACATTAATCTGTAGTGTGGCAGGTGATCCGGTTCCTAA	1031
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VERSION
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SOURCE
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3194)
AUTHORS Shelton,D.L., Sutherland,J., Gripp,J., Camerato,T., Armanini,M.P.,
Phillips,H.S., Carroll,K., Spencer,S.D. and Levinson,A.D.
TITLE Human trks: molecular cloning, tissue distribution, and expression
of extracellular domain immunoadhesins
J Neurosci. 15 (1 Pt 2), 477-491 (1995)
JOURNAL
MEDLINE 56123473
PUBMED 7823156
REMARK GenBank staff at the National Library of Medicine created this
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Matches 3162; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2610)
AUTHORS Wu,J., Zhang,B., Zhou,Y., Peng,X., Yuan,J. and Qiang,B.
TITLE Direct Submision
JOURNAL Submitted (18-JUL-2001) Department of Biochemistry, Institute of Basic Medical Science, Chinese Academy of Medical Sciences and Peking Union Medical College, 5 Dong Dan San Tiao, Beijing 100005, P.R. China
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AUTHORS Godowski, P.J., Mark, M.R., Sadick, M.D., Shelton, D.L. and
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DEFINITION Sequence 6 from patent US 6287784.
ACCESSION AR168009
VERSION AR168009.1 GI:17903824
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 3060)
AUTHORS Godowski, P.J., Marx, M.R., Sadick, M. Daniel, and Wong, W. Lee, Tan.
TITLE Kinase receptor activation assay
JOURNAL Patent: US 6287784-A 6.11-SEP-2001;
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AX683038
LOCUS AX683038 4757 bp DNA linear PAT 29-MAR-2003
DEFINITION Sequence 12 from Patent EP1297944.
ACCESSION AX683038
VERSION AX683038.1 GI:29370110
KEYWORDS Rattus norvegicus (Norway rat)

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DEFINITION cdg.
ACCESSION M55291
VERSION M55291.1 GI:207473
KEYWORDS neural receptor protein-tyrosine kinase.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 4757)
AUTHORS Middlemas,D.S., Lindberg,R.A. and Hunter,T.
TITLE trkb, a neural receptor protein-tyrosine kinase: evidence for a
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JOURNAL Mol. Cell. Biol. 11 (1), 143-153 (1991)
MEDLINE 91094826
PUBMED 1846020
COMMENT Original source text: Rat (Sprague-Dawley) adult cerebellum, cDNA
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LOCUS Murine trkB mRNA for tyrosine protein kinase receptor.
DEFINITION X17647
ACCESSION X17647
VERSION X17647.1 GI:55505
KEYWORDS Kinase; protein kinase; receptor; transmembrane protein; trkB gene;
tyrosine kinase.
SOURCE Mus sp.
ORGANISM Mus sp.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 4351)
AUTHORS Klein,R., Parada,L.F., Coulter,F. and Barbacid,M.
TITLE trkB, a novel tyrosine protein kinase receptor expressed during
mouse neural development
JOURNAL EMBO J. 8 (12), 3701-3709 (1989)
MEDLINE 90059970
PUBMED 255172
REFERENCE 2 (bases 1 to 4351)
AUTHORS Klein,R., Parada,L.F., Coulter,F. and Barbacid,M.
TITLE Direct Submission
JOURNAL Submitted (22-MAR-1990)
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ORIGIN

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Matches 2671; Conservative 0; Mismatches 521; Indels 45; Gaps 12;

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LOCUS
DEFINITION Sequence 1 from patent US 5622862.
ACCESSION 140971

VERSION 140971.1 GI:2082451
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2463)
AUTHORS Squitro,S.P., Glass,D., Aldrich,T.H., Distefano,P., Stitt,T.,
Futuh,M.E. and Yancopoulos,G.D.
TITLE Assay systems for erbB neurotrophin activity
JOURNAL Patent: US 5622862-A 1 22-APR-1997;
FEATURES
source Location/Qualifiers
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Best Local Similarity 87.5%; Pred. No. 0;
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ACCESSION CO723213
VERSION CO723213.1 GI:42284070
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,B.W.
TITLE Kites, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 9147 06-SEP-2002;
PUB Corporation (NY) (US)
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XX Brodeur GM, Nakagawara A;
XX WPI; 1996-097583/10.
XX Nucleic acid encoding human neurotrophic factor receptor. TRK-B - used to
XX develop primers and antibodies for use in assays to determine
XX aggressiveness of neuroblastoma tumours.
XX Claim 1; Page 37-39; sipp; English.
XX The cDNA encodes a full length human neurotrophic factor receptor TRK-B.
XX TRK-B is a receptor for brain-derived neurotrophic factor but it also
XX binds neurotrophin-3 and -4/5. The cDNA can be used to express the full
XX length protein and to design primers for detection of the presence of TRK
XX -B transcripts in cells. Antisense oligonucleotides can be used to
XX inhibit the expression of TRK-B in neuroblastomas
XX
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Dp	1981	CTAAGCGAAGAGACCTTTGGAAAAAGTGTCTTCAAGTGAATGCTATTAACCTCTGTCTGAG	2040
QY	2041	CAGGACAAAGATCTTGGTGGCAGTGAAGAACCCTGAAGATGCGCAGTGAACAATGACGCAAG	2100
Dp	2041	CAGGACAAAGATCTTGGTGGCAGTGAAGAACCCTGAAGATGCGCAGTGAACAATGACGCAAG	2100
QY	2101	GACTTCCACCGTGAAGGCCGAGCTCTGTACCAACTCTCCAGCATGACATGCTCAATTC	2160
Dp	2101	GACTTCCACCGTGAAGGCCGAGCTCTGTACCAACTCTCCAGCATGACATGCTCAATTC	2160
QY	2161	TATGGCGCTCGTGGAGGAGGACCCCCCTCATATGCTCTTGTAGTACATGAAGATGGG	2220
Dp	2161	TATGGCGCTCGTGGAGGAGGACCCCCCTCATATGCTCTTGTAGTACATGAAGATGGG	2220
QY	2221	GACCTCAACAAAGTTCCTCAGGGGCAACCGGCCCTGTATGCGCTGATGGCTGAAGGGCAAC	2280
Dp	2221	GACCTCAACAAAGTTCCTCAGGGGCAACCGGCCCTGTATGCGCTGATGGCTGAAGGGCAAC	2280
QY	2281	CCGCCCAACGGAACTGACGCAAGTCCGAGATGCTGTCAATAGCCCAAGCATGCGCGCGGAC	2340
Dp	2281	CCGCCCAACGGAACTGACGCAAGTCCGAGATGCTGTCAATAGCCCAAGCATGCGCGCGGAC	2340
QY	2341	ATGGCTTACCTGAGGCTGCCAGACCTTGCTGTGACCGCGCATTTGGCCACAGGAACGTGCTG	2400
Dp	2341	ATGGCTTACCTGAGGCTGCCAGACCTTGCTGTGACCGCGCATTTGGCCACAGGAACGTGCTG	2400
QY	2401	GTCCGGGAGAACTTGCTGTGTGAAAATCCGGGACCTTTGGGAATGTCCCGGGAAGTGTACACG	2460
Dp	2401	GTCCGGGAGAACTTGCTGTGTGAAAATCCGGGGAATGTCCCGGGAAGTGTGTACACG	2460
QY	2461	ACTGACTTACAGAGGTCGTGTGGCCACAATGCTGTGCCATTCGTGTGATGCTTCCAGAG	2520
Dp	2461	ACTGACTTACAGAGGTCGTGTGGCCACAATGCTGTGCCATTCGTGTGATGCTTCCAGAG	2520
QY	2521	AGCATCAATGTACAGGAATTTCAACACCGAAGCCAGCTGTGAGCTGTGGGGGTGTGTGG	2580
Dp	2521	AGCATCAATGTACAGGAATTTCAACACCGAAGCCAGCTGTGAGCTGTGGGGGTGTGTGG	2580
QY	2581	TGGGAGATTTTCACTTATGGCAAAACAGGCTGTGTACAGCTGTCAAAACAATGAGGTGTA	2640
Dp	2581	TGGGAGATTTTCACTTATGGCAAAACAGGCTGTGTACAGCTGTCAAAACAATGAGGTGTA	2640
QY	2641	GAGTGTATCACTCAGGGCCGAGTCTGTGACGACCCCGGACGTCGCCCAGAGAGTGTAT	2700
Dp	2641	GAGTGTATCACTCAGGGCCGAGTCTGTGACGACCCCGGACGTCGCCCAGAGAGTGTAT	2700
QY	2701	GAGCTGAATGTCTGGGGTGTGTGCAAGGAAGCCCAATGAGGAAGAAATCAAGGGCATC	2760
Dp	2701	GAGCTGAATGTCTGGGGTGTGTGCAAGGAAGCCCAATGAGGAAGAAATCAAGGGCATC	2760
QY	2761	CATACCTCTCTTCAGAACTTGGCCAAAGGCATTCGCGTCTACCTGTGAATTTCTAGGCTAG	2820
Dp	2761	CATACCTCTCTTCAGAACTTGGCCAAAGGCATTCGCGTCTACCTGTGAATTTCTAGGCTAG	2820
QY	2821	GGCCCTTTTCCCAAGCCGATCTTCCCAAGCTACTCTCAAGCGGGCTGAGAGATGA	2880

Db	2821	GGCCCTTTTCCCGACCGATCTTCCCAAGTACTCTGAGCGGGCTGAGAGATGAA	2880
Qy	2881	CATCTTTTAACTGCGCGCTGAGAGGCCAACAGCTGCTCTTCACTGTGACATATTAAAC	2940
Db	2881	CATCTTTTAACTGCGCGCTGAGAGGCCAACAGCTGCTCTCTTCACTGTGACATATTAAAC	2940
Qy	2941	ATCAAAAGCTCCGGAAGCTCTCGAGGGAAAGAGTGTACTTTTATCATCATGACACA	3000
Db	2941	ATCAAAAGCTCCGGAAGCTCTCGAGGGAAAGAGTGTACTTTTATCATCATGACACA	3000
Qy	3001	GAATTGACTTCTTTTGGCATTAATCTCTTCTCTCTTCCATCTCCCTGGTGTGCTT	3060
Db	3001	GAATTGACTTCTTTTGGCATTAATCTCTTCTCTCTTCCATCTCCCTGGTGTGCTT	3060
Qy	3061	TTTCTTTTAAATTTTCTTTTCTTCTTTTGTCTCTCCCTGCTTCAGATTCCT	3120
Db	3061	TTTCTTTTAAATTTTCTTTTCTTCTTTTGTCTCTCCCTGCTTCAGATTCCT	3120
Qy	3121	ACCCTTTCTTTGATCAATCTGGCTTCTGATTAATTAATCTGTGACATGACAAAGGC	3180
Db	3121	ACCCTTTCTTTGATCAATCTGGCTTCTGATTAATTAATCTGTGACATGACAAAGGC	3180
Qy	3181	CTTAAACAAAGTAATTTGTTATATACAGACACAATCGAGTTGGCCACCAACTAACAA	3240
Db	3181	CTTAAACAAAGTAATTTGTTATATACAGACACATCGAGTTGGCCACCAACTAACAA	3240
Qy	3241	TGCTTGTGTATTCCTGCTTGTATGTGATGTAAGGAAAGGAAACAAATATTTCCT	3300
Db	3241	TGCTTGTGTATTCCTGCTTGTATGTGATGTAAGGAAAGGAAACAAATATTTCCT	3300
Qy	3301	TAAACTTTGTCACTTCTGCTGTAACAGATATGAGAGTTTCTAGATTCATTTTAA	3360
Db	3301	TAAACTTTGTCACTTCTGCTGTAACAGATATGAGAGTTTCTAGATTCATTTTAA	3360
Qy	3361	TTTATTAATTAATCACTGTTCTTATTTGTTTGGATGAGCTTAAAGCTGTGTATTAAGAA	3420
Db	3361	TTTATTAATTAATCACTGTTCTTATTTGTTTGGATGAGCTTAAAGCTGTGTATTAAGAA	3420
Qy	3421	AACTTGTGTCAATCTGTAAGCCTTTATCTATGTGGAGATTTAAACAGAGAGAAAG	3480
Db	3421	AACTTGTGTCAATCTGTAAGCCTTTATCTATGTGGAGATTTAAACAGAGAGAAAG	3480
Qy	3481	ATTATTAATGAACCGCAATATGAGAGAAACAAGACAACAATCTGGATTCAGCTGTGCA	3540
Db	3481	ATTATTAATGAACCGCAATATGAGAGAAACAAGACAACAATCTGGATTCAGCTGTGCA	3540
Qy	3541	GTCCTTACTTGGAAATATCTGAGCACTGTTAGCTGGAAAGATGTATTGGGCACTTCC	3600
Db	3541	GTCCTTACTTGGAAATATCTGAGCACTGTTAGCTGGAAAGATGTATTGGGCACTTCC	3600
Qy	3601	CTGAGAGCCTTCTGAGAGATTAAGAAAGACTACTGAGGCTGTGTCATGATGATTCCTT	3660
Db	3601	CTGAGAGCCTTCTGAGAGATTAAGAAAGACTACTGAGGCTGTGTCATGATGATTCCTT	3660
Qy	3661	TCCCATCACCAAGATGATGCTGCGTAGAGGCAAAAGTGGCTT 3707	
Db	3661	TCCCATCACCAAGATGATGCTGCGTAGAGGCAAAAGTGGCTT 3707	
RESULT 2			
AAD45786			
ID AAD45786 standard; DNA; 3707 BP.			
AC AAD45786;			
XX			
XX 27-DEC-2002 (first entry)			
XX			
DE Human TrkB DNA.			
KW Human, neurodegenerative disorder; neurodevelopmental disorder; TrkB;			
TK; Alzheimer's disease; AD; amyotrophic lateral sclerosis; ALS; PD;			
Parkinson's disease; Huntington's disease; HD; Lou Gehrig's disease;			

KM diabetic peripheral neuropathy; Down's syndrome; DS; neuroprotective;
 KM gene therapy; anticonvulsant; cerebroprotective; neurotropic; gene; ds.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 XX Key 352.. 2820
 XX CDS /tag= a
 XX /product= "Human TrkB protein"
 FT MO200267858-A2.
 PN 06-SBP-2002.
 PD 22-FEB-2002; 2002MO-US005151.
 PF 22-FEB-2001; 2001US-0270553P.
 PR (UWMA-) UNIV MARYLAND BALTIMORE.
 PA Krueger BK, Kingsbury TJ, Bambrick LJ, Dorsey SG,
 PI MPI; 2002-698627/75.
 DR P-PSDB; AAE27931.
 XX Treating and/or preventing neurodegenerative and neurodevelopmental
 PT disorders such as Alzheimer's, Parkinson's and Huntington's diseases by
 PT altering the ratio of amount of full-length and truncated TrkB or TrkC
 PT polypeptides.
 XX Disclousure; Page 54-56; 96pp; English.
 XX The present invention relates to a method of treating neurodegenerative
 CC or neurodevelopmental disorders in a mammal which involves administering
 CC an isolated nucleic acid encoding a full-length TrkB or TrkC or their
 CC mutant, variant, homologue or fragment or an anti-sense RNA for truncated
 CC TrkB or TrkC isoforms, where they increase the amount of full-length TrkB
 CC or TrkC or decrease the amount of truncated TrkB or TrkC in treated
 CC neurons. The methods and compositions of the invention are useful for
 CC treating or preventing neurodegenerative or neurodevelopmental disorders
 CC such as Alzheimer's disease (AD), Parkinson's disease (PD), Huntington's
 CC disease (HD), amyotrophic lateral sclerosis (ALS; Lou Gehrig's disease),
 CC diabetic peripheral neuropathy, the adverse complications of Down's
 CC syndrome (DS) and other types of peripheral neuropathy. Sequences of the
 CC invention are also used in gene therapy. The present sequence is human
 CC TrkB DNA
 XX
 SQ Sequence 3707 BP; 942 A; 948 C; 900 G; 917 T; 0 U; 0 Other;
 Query Match 100.0%; Score 3707; DB 6; Length 3707;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 CCGCCGCTGACAGCGCGGAGCAGGCACTCGGCGTGGCACTGGCTAGGGAATGTCGTC 360
 Db 301 CCGCGGCTGACAGCGCGGAGCAGGCACTCGGCGTGGCACTGGCTAGGGAATGTCGTC 360
 QY 361 TGGATTAAGTGGCATGAGACCGGCATGACGCGCTCTGCGGCTTGTGCTGCTGTTGTG 420
 Db 361 TGGATTAAGTGGCATGAGACCGGCATGACGCGCTCTGCGGCTTGTGCTGCTGTTGTG 420
 QY 421 GGCCTTGGAGGCGCGCTTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 Db 421 GGCCTTGGAGGCGCGCTTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 QY 481 TGGTGACGAGACCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
 Db 481 TGGTGACGAGACCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
 QY 541 GATCCTGAGAACATCACCGAAATTTTCATGCAAAACGAAAGGTTAGAAATCATCAAC 600
 Db 541 GATCCTGAGAACATCACCGAAATTTTCATGCAAAACGAAAGGTTAGAAATCATCAAC 600
 QY 601 GAAGATGATGTTGAAGCTTATGTTGGACTGAGAAATCTGCAATTTGGAATTTGATTA 660
 Db 601 GAAGATGATGTTGAAGCTTATGTTGGACTGAGAAATCTGCAATTTGGAATTTGATTA 660
 QY 661 AAATTTGGCTCATTAAGCATTTCTGAAAGAAACAGCAACCTGACGACATCAATTTACC 720
 Db 661 AAATTTGGCTCATTAAGCATTTCTGAAAGAAACAGCAACCTGACGACATCAATTTACC 720
 QY 721 CGAAACAACTGACGAGTTGTCTAGAGAAACATTTCCGTCACCTTGACTGTGTAAC 780
 Db 721 CGAAACAACTGACGAGTTGTCTAGAGAAACATTTCCGTCACCTTGACTGTGTAAC 780
 QY 781 ATCTGCTGGGCAATTCATTTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 Db 781 ATCTGCTGGGCAATTCATTTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 QY 841 GAGGCTTAATCCAGTCCAGACCTGAGGATTTGATGCTGCTGCTGCTGCTGCTGCTGCTG 900
 Db 841 GAGGCTTAATCCAGTCCAGACCTGAGGATTTGATGCTGCTGCTGCTGCTGCTGCTGCTG 900
 QY 901 ATTCCCTGGCAAACTGACGATACCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 Db 901 ATTCCCTGGCAAACTGACGATACCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 QY 961 CTTAACCCTGCTGAGGAGGAAAGTCTATCATATTCCTGATGCTGCTGCTGCTGCTGCTG 1020
 Db 961 CTTAACCCTGCTGAGGAGGAAAGTCTATCATATTCCTGATGCTGCTGCTGCTGCTGCTG 1020
 QY 1021 CCGGTTCTTAATATGATTTGGGATGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
 Db 1021 CCGGTTCTTAATATGATTTGGGATGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
 QY 1081 AGGCACACAGGCGCTCTTAAGGATTAATCAATTTCAATCCATGACATGAGTGGAGACAG 1140
 Db 1081 AGGCACACAGGCGCTCTTAAGGATTAATCAATTTCAATCCATGACATGAGTGGAGACAG 1140
 QY 1141 ATCTTGTGTGGGGAATTTTGTAGAGAGATCAAGATTCGTCAACCTCACTGTG 1200
 Db 1141 ATCTTGTGTGGGGAATTTTGTAGAGAGATCAAGATTCGTCAACCTCACTGTG 1200
 QY 1201 CATTTTGACCAATATCAATTTCTGAAATTCGAACTTCGACACCACTGTTGATTT 1260
 Db 1201 CATTTTGACCAATATCAATTTCTGAAATTCGAACTTCGACACCACTGTTGATTT 1260
 QY 1261 CCATTGCACTGTAAGGCAACCCCAACAGCGCTTCAAGTGTCTTAACCGGGCAATA 1320
 Db 1261 CCATTGCACTGTAAGGCAACCCCAACAGCGCTTCAAGTGTCTTAACCGGGCAATA 1320
 QY 1321 TTGAATGATCCAAATATCATCTGATTAATATCATGTTTCAATCAACGAGATACAC 1380
 Db 1321 TTGAATGATCCAAATATCATCTGATTAATATCATGTTTCAATCAACGAGATACAC 1380
 QY 1381 GGCCTGCTCAAGCTGATTAATCCATCAATGAACAATGGGAGCTACCTTAATAGCC 1440

Db	1361	GGCTCCCTCCACGCTGGATTAATCCACTCAACGAAACAATGGGGACTTACAACCTTAATACCC	1440
Qy	1441	AAGAATGATGATGGGAGGATGAGAAACAGATTTCTGCTCACTTATGGGCTGGCTGGA	1500
Db	1441	AAGAATGATGATGGGAGGATGAGAAACAGATTTCTGCTCACTTATGGGCTGGCTGGA	1500
Qy	1501	ATTGACGATGGTCAAAACCCAAATTTATCTGATGTAATTTATGAAATTAATGAACTGCA	1560
Db	1501	ATTGACGATGGTCAAAACCCAAATTTATCTGATGTAATTTATGAAATTAATGAACTGCA	1560
Qy	1561	GGGAATGACATCGGGGACACACGAAACAGAGTAATGAAATCCCTTCCACAGACGTCACT	1620
Db	1561	GGGAATGACATCGGGGACACACGAAACAGAGTAATGAAATCCCTTCCACAGACGTCACT	1620
Qy	1621	GATTAACACCGGTCGGGAAACATCTCGGCTATGCTGAGTGAGTAATGGCGTCTGTGTG	1680
Db	1621	GATTAACACCGGTCGGGAAACATCTCGGCTATGCTGAGTGAGTAATGGCGTCTGTGTG	1680
Qy	1681	GGATTTTGCCTTTTGGTAATGCTGTTTCTGTTAAGTTGGACAGACACTCCAAAGTTTGGC	1740
Db	1681	GGATTTTGCCTTTTGGTAATGCTGTTTCTGTTAAGTTGGACAGACACTCCAAAGTTTGGC	1740
Qy	1741	ATGAAAGGCCACAGCCTCCGTTATCAGCAATGATGATGACTCTGCCAGCCCACTCCATCAC	1800
Db	1741	ATGAAAGGCCACAGCCTCCGTTATCAGCAATGATGATGACTCTGCCAGCCCACTCCATCAC	1800
Qy	1801	ATCTCCAAATGGGAGTACACTCATCTTCTTGGAAAGTGGCCAGATGCTGTCAATT	1860
Db	1801	ATCTCCAAATGGGAGTACACTCATCTTCTTGGAAAGTGGCCAGATGCTGTCAATT	1860
Qy	1861	GGAAATGACCAAGATCCCTGTCAATTGAAATCCCGAGTACTTGGCATCAACCAAGTCAG	1920
Db	1861	GGAAATGACCAAGATCCCTGTCAATTGAAATCCCGAGTACTTGGCATCAACCAAGTCAG	1920
Qy	1921	CTCAAAGCAGACACATTTGTTACAGACATCAAGGACATTAACATTTGTTCTGAAAGGAG	1980
Db	1921	CTCAAAGCAGACACATTTGTTACAGACATCAAGGACATTAACATTTGTTCTGAAAGGAG	1980
Qy	1981	CTAAGGCGAAGAGCCTTTGGAAGATGTTTCCAGTGAATGTAATTAACCTGTCTCTAG	2040
Db	1981	CTAAGGCGAAGAGCCTTTGGAAGATGTTTCCAGTGAATGTAATTAACCTGTCTCTAG	2040
Qy	2041	CAGACCAAGATCTTGGTGGCAGTGAAGACCTTGAAGATGCGACATGACAGCAAG	2100
Db	2041	CAGACCAAGATCTTGGTGGCAGTGAAGACCTTGAAGATGCGACATGACAGCAAG	2100
Qy	2101	GACTTCCACCGTGAAGGCGAGGCTCTGACCAACCTCGACATGAGCAATCGTCAAGTTTC	2160
Db	2101	GACTTCCACCGTGAAGGCGAGGCTCTGACCAACCTCGACATGAGCAATCGTCAAGTTTC	2160
Qy	2161	TATGGCGTCTCGTGGAGGAGGAGACCCCTCATCAATGATCTTTGATACATGAAGATGGG	2220
Db	2161	TATGGCGTCTCGTGGAGGAGGAGACCCCTCATCAATGATCTTTGATACATGAAGATGGG	2220
Qy	2221	GACCTCAACAAGTTCTCTGAGGGGACACGAGCCCTGATGCGTGTGATGGCTGAGGGCAAC	2280
Db	2221	GACCTCAACAAGTTCTCTGAGGGGACACGAGCCCTGATGCGTGTGATGGCTGAGGGCAAC	2280
Qy	2281	CCGCCCAACGGAATGACGCAAGTCGAGATGCTGATATATAGCCACAGACATCGCCGGGAC	2340
Db	2281	CCGCCCAACGGAATGACGCAAGTCGAGATGCTGATATATAGCCACAGACATCGCCGGGAC	2340
Qy	2341	ATGCTCTACCTGCGCTCCACAGACTTGTGACACCGGCAATTTGGCCACAGAACTGCTGTG	2400
Db	2341	ATGCTCTACCTGCGCTCCACAGACTTGTGACACCGGCAATTTGGCCACAGAACTGCTGTG	2400
Qy	2401	GTCGGGAGAACTTGTCTGTGTAATAATCGGGGACTTGGGATGTCCCGGAGAGTGTACAGC	2460
Db	2401	GTCGGGAGAACTTGTCTGTGTAATAATCGGGGACTTGGGATGTCCCGGAGAGTGTACAGC	2460
Qy	2461	ACTGACTACTACAGGCTCGTGGCCACAACAATGCTGCCATTTGCTGTGATGCTTCCAGAG	2520
Db	2461	ACTGACTACTACAGGCTCGTGGCCACAACAATGCTGCCATTTGCTGTGATGCTTCCAGAG	2520
Qy	2521	AGCATCAATGTAACAGAAATTTCAACGACGGAAAGCGACGCTGTGAGACTGTGGGGTCTGTG	2580
Db	2521	AGCATCAATGTAACAGAAATTTCAACGACGGAAAGCGACGCTGTGAGACTGTGGGGTCTGTG	2580
Qy	2581	TGGAGATTTTTCACTATGCGAAACAGCCCTGTGATACAGCTGTCAAAACAATGAGGTGTA	2640
Db	2581	TGGAGATTTTTCACTATGCGAAACAGCCCTGTGATACAGCTGTGTCAAAACAATGAGGTGTA	2640
Qy	2641	GAGGTATCACTACAGGGCCGAGTCTCTGAGCGACCCCGCACGTGCCCTCCAGAGGTGTAT	2700
Db	2641	GAGGTATCACTACAGGGCCGAGTCTCTGAGCGACCCCGCACGTGCCCTCCAGAGGTGTAT	2700
Qy	2701	GAGCTGATGCTGGGGTCTGGCAGCGAGGCCCCACATGAGGAACAATCAAGGGGATC	2760
Db	2701	GAGCTGATGCTGGGGTCTGGCAGCGAGGCCCCACATGAGGAACAATCAAGGGGATC	2760
Qy	2761	CATACCTCTCTTGAAACTTGGCCCAAGGCAATCTCCGCTTACCTGACATTTAGGCTAG	2820
Db	2761	CATACCTCTCTTGAAACTTGGCCCAAGGCAATCTCCGCTTACCTGACATTTAGGCTAG	2820
Qy	2821	GGCCCTTTTCCCGACAGCCGATCTTCCCAAGTACTCTCAGAGCGGCTGAGAGATGAA	2880
Db	2821	GGCCCTTTTCCCGACAGCCGATCTTCCCAAGTACTCTCAGAGCGGCTGAGAGATGAA	2880
Qy	2881	CATCTTTTAACCTGCGGTCGAGAGGCGCACCAAGGCTCTCCCTTCACTGTGACAGATTAC	2940
Db	2881	CATCTTTTAACCTGCGGTCGAGAGGCGCACCAAGGCTCTCCCTTCACTGTGACAGATTAC	2940
Qy	2941	ATCAAGAATCCGAGAAAGCTCTCGAGGGGAAGCAGTGTGTACTTTTCATCCATGAGACCA	3000
Db	2941	ATCAAGAATCCGAGAAAGCTCTCGAGGGGAAGCAGTGTGTACTTTTCATCCATGAGACCA	3000
Qy	3001	GTATGACTCTTTTGGCAATTAATCTCTTCTCTCTTCCATCTCCCTGGTGTCTCT	3060
Db	3001	GTATGACTCTTTTGGCAATTAATCTCTTCTCTCTTCCATCTCCCTGGTGTCTCT	3060
Qy	3061	TTTCTTTTAAATTTCTCTTTTCTCTTTTGGTGTGCTGCCCTGACAGATTCT	3120
Db	3061	TTTCTTTTAAATTTCTCTTTTCTCTTTTGGTGTGCTGCCCTGACAGATTCT	3120
Qy	3121	ACCCTTCTTTTGATCAATCTGGCTCTGCACTTACTATTAACTCTGATGACAAAGGC	3180
Db	3121	ACCCTTCTTTTGATCAATCTGGCTCTGCACTTACTATTAACTCTGATGACAAAGGC	3180
Qy	3181	CTTAACAACGTAATTTGTTATATCAGCAGACACTCGCAGTTTGGCCACCAACTTAACA	3240
Db	3181	CTTAACAACGTAATTTGTTATATCAGCAGACACTCGCAGTTTGGCCACCAACTTAACA	3240
Qy	3241	TGCGTGTGTGATTTCCGCGCTTTGATGTGATGATAAAAAAGGAAACAATATTTCACT	3300
Db	3241	TGCGTGTGTGATTTCCGCGCTTTGATGTGATGATAAAAAAGGAAACAATATTTCACT	3300
Qy	3301	TAAACTTTGTCACTTCTGCTGTACAGATATCGAGATTTCTATGAGATTCACTTATTTA	3360
Db	3301	TAAACTTTGTCACTTCTGCTGTACAGATATCGAGATTTCTATGAGATTCACTTATTTA	3360
Qy	3361	TTTATTTATTAATCTGTTCTTAATTTGTTTGGATGCTTAAGCCTGTGTATTAAGAA	3420
Db	3361	TTTATTTATTAATCTGTTCTTAATTTGTTTGGATGCTTAAGCCTGTGTATTAAGAA	3420
Qy	3421	AACTTGATCAATCTGTGAAGCCTTATCTATGAGGAGTTAAACCAAGAGAAACAG	3480
Db	3421	AACTTGATCAATCTGTGAAGCCTTATCTATGAGGAGTTAAACCAAGAGAAACAG	3480
Qy	3481	ATTATTAATGAACCGCAATATGGGAGGACAAAGACACTGAGATCTGATCTGTGTCA	3540
Db	3481	ATTATTAATGAACCGCAATATGGGAGGACAAAGACACTGAGATCTGATCTGTGTCA	3540
Qy	3541	GTCCTTACTTGAAGAAATCTCAGCAACTGTTAGCTGGAGAAATGTAATTGGCACTTTC	3600
Db	3541	GTCCTTACTTGAAGAAATCTCAGCAACTGTTAGCTGGAGAAATGTAATTGGCACTTTC	3600

Db 961 CTTAACTGCTGGAGGAAAGCTATCACTTATCTGTAGTGGCAGGTAT 1020
Qy 1021 CCGGTTCCATATATATATTTGGGATGTTGGTAACCTGGTTTCCAAACATATGATGAACA 1080
Db 1021 CCGGTTCCATATATATATTTGGGATGTTGGTAACCTGGTTTCCAAACATATGATGAACA 1080
Qy 1081 AGCCACACACAGGGCTCTTAAGGATTAATACTATTCATCCGATGACAGTGGGAGCAG 1140
Db 1081 AGCCACACACAGGGCTCTTAAGGATTAATACTATTCATCCGATGACAGTGGGAGCAG 1140
Qy 1141 ATCTTGTGTGGGGGAAATCTTGTAGGAGAAATCAAGATTCGTCAACTCACTGTG 1200
Db 1141 ATCTTGTGTGGGGGAAATCTTGTAGGAGAAATCAAGATTCGTCAACTCACTGTG 1200
Qy 1201 CATTTGGACCACTATCACTTCTCGAATCTCGAACCTCGAACCACTGGGCACTT 1260
Db 1201 CATTTGGACCACTATCACTTCTCGAATCTCGAACCTCGAACCACTGGGCACTT 1260
Qy 1261 CCATTCACCTGTGAAGGCAACCCCAACCAAGGCTTCAAGTGTCTATTAAGGGGCAATA 1320
Db 1261 CCATTCACCTGTGAAGGCAACCCCAACCAAGGCTTCAAGTGTCTATTAAGGGGCAATA 1320
Qy 1321 TTGAATGATCCAAATATCATCTGTATCTAATAATACATGTTACCAATCACAGAGTACAC 1380
Db 1321 TTGAATGATCCAAATATCATCTGTATCTAATAATACATGTTACCAATCACAGAGTACAC 1380
Qy 1381 GGGCTCCCTCCAGCTGGAGTAATCCCACTGACATGAACATGGGGACTAATCTTAATAGCC 1440
Db 1381 GGGCTCCCTCCAGCTGGAGTAATCCCACTGACATGAACATGGGGACTAATCTTAATAGCC 1440
Qy 1441 AAGAATGATATGGGAAAGATGAGAAACAGATTTCTGCTCACTTCACTGGGCTGGCTGGA 1500
Db 1441 AAGAATGATATGGGAAAGATGAGAAACAGATTTCTGCTCACTTCACTGGGCTGGCTGGA 1500
Qy 1501 ATTTGATGATGTCGCAACCCCAATTTATCTGATGTAATTTATGAAATTTATGAACTGCA 1560
Db 1501 ATTTGATGATGTCGCAACCCCAATTTATCTGATGTAATTTATGAAATTTATGAACTGCA 1560
Qy 1561 GCGAATGATCTGGGGGACCAACGAAAGAAATGAAATCCCTTCCACAGAGCTGACT 1620
Db 1561 GCGAATGATCTGGGGGACCAACGAAAGAAATGAAATCCCTTCCACAGAGCTGACT 1620
Qy 1621 GATTAACCCGCTGGGAAATCTCTCGGTATGCTGTGATGATGATGATGATGATGATGATG 1680
Db 1621 GATTAACCCGCTGGGAAATCTCTCGGTATGCTGTGATGATGATGATGATGATGATGATG 1680
Qy 1681 GGAATTTGCTTTTGTGTAATGCTGTTTCTGCTTAAAGTTGGCAAGACATCCAGTTTGGC 1740
Db 1681 GGAATTTGCTTTTGTGTAATGCTGTTTCTGCTTAAAGTTGGCAAGACATCCAGTTTGGC 1740
Qy 1741 ATGAAGGCCCAAGCTCTGTTATCAGCAATGATGATGATGATGATGATGATGATGATGATG 1800
Db 1741 ATGAAGGCCCAAGCTCTGTTATCAGCAATGATGATGATGATGATGATGATGATGATGATG 1800
Qy 1801 ATCTCCAAATGGGAGTAACATCCACTCTTCGGAAGGTGGCCGAGATGCTGATTAAT 1860
Db 1801 ATCTCCAAATGGGAGTAACATCCACTCTTCGGAAGGTGGCCGAGATGCTGATTAAT 1860
Qy 1861 GGAATGACCAAGATCCCTGATTTGAAATCCCAAGTCTTTGGCATCAACCAAGTCAAG 1920
Db 1861 GGAATGACCAAGATCCCTGATTTGAAATCCCAAGTCTTTGGCATCAACCAAGTCAAG 1920
Qy 1921 CTCAAGCCAGACATTTGTTTCAAGCAATCAAGGCAATTAATGTTCTGTAAGGAGGAG 1980
Db 1921 CTCAAGCCAGACATTTGTTTCAAGCAATCAAGGCAATTAATGTTCTGTAAGGAGGAG 1980
Qy 1981 CTAGGCGAAGAGCTTTGAAAGTGTCTAGTGAATGCTAATACCTGCTGCTGAG 2040
Db 1981 CTAGGCGAAGAGCTTTGAAAGTGTCTAGTGAATGCTAATACCTGCTGCTGAG 2040
Qy 2041 CAGGACGAATCTTGTGAGTGAAGACCTGAAGATGCGAGTGAATGCAAGCAG 2100
Db 2041 CAGGACGAATCTTGTGAGTGAAGACCTGAAGATGCGAGTGAATGCAAGCAG 2100

Db 2041 CAGGACGAATCTTGTGAGTGAAGACCTGAAGATGCGAGTGAATGCAAGCAG 2100
Qy 2101 GACTTCCACCGTGAAGGCGGAGCTCTGACCAACCTTCAGATGAGCATGCTGAAGTTTC 2160
Db 2101 GACTTCCACCGTGAAGGCGGAGCTCTGACCAACCTTCAGATGAGCATGCTGAAGTTTC 2160
Qy 2161 TATGGCTCTGCTGAGAGGGGACCCCTCATCATGTCTTTGATCATGAGCATGAGG 2220
Db 2161 TATGGCTCTGCTGAGAGGGGACCCCTCATCATGTCTTTGATCATGAGCATGAGG 2220
Qy 2221 GACCTCAACAAAGTCTTCAAGGGGACAGGGGCTGATGCGGTGATGAGGCTGAGGAGC 2280
Db 2221 GACCTCAACAAAGTCTTCAAGGGGACAGGGGCTGATGCGGTGATGAGGCTGAGGAGC 2280
Qy 2281 CCGCCACGGAATGACGAGCTGCAATGCTGATATAGCCACAGATGCGCGGGC 2340
Db 2281 CCGCCACGGAATGACGAGCTGCAATGCTGATATAGCCACAGATGCGCGGGC 2340
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Db 2941 ATCAAAAGCTCCGAAAGCTCTGAGGGAAGCAGTGTATCTTCTTCAATCCATGAGACA 3000
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Db      3061 TTTCTTTTAAATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 3120
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Qy      3241 TGCCTGTGTGATCTCGCTTGTATGATGATGATGATGATGATGATGATGATGATGAT 3300
Db      3241 TGCCTGTGTGATCTCGCTTGTATGATGATGATGATGATGATGATGATGATGATGAT 3300
Qy      3301 TAAACCTTGACACTCTGCTGTACAGATTCGAGAGTTTCTATGATTCATCTTATTTA 3360
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Qy      3361 TTTATTTATTTACTGTTCTTATTTGTTTGTGATGCTTAAAGCTGTATTTAAAAAGAA 3420
Db      3361 TTTATTTATTTACTGTTCTTATTTGTTTGTGATGCTTAAAGCTGTATTTAAAAAGAA 3420
Qy      3421 AACTGTGTGATCTGTGAAAGCTTTATCTATGAGAGATTTAAACAGAGAGAAAGAG 3480
Db      3421 AACTGTGTGATCTGTGAAAGCTTTATCTATGAGAGATTTAAACAGAGAGAAAGAG 3480
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Db      3481 ATTATTTATGAGCGCAATATGAGGAGAAACAACAACCTGGATGCTGGTGTCA 3540
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Db      3541 GTCCCTACTTGAAGAAATCTGAGCACTGTAGCTGGGAAAGATGTATTCGGACCTTCC 3600
Qy      3601 CTGAGAGACTTTCTGAGAGATGAGAGTAAAGACTAGCGCTGTCCATGATGATCTTT 3660
Db      3601 CTGAGAGACTTTCTGAGAGATGAGAGTAAAGACTAGCGCTGTCCATGATGATCTTT 3660
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Db      3661 TCCCATACCAAGAAATGATAGCGTGCAGTAGAGCAAAAGTGGCTT 3707

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RESULT 5
ADE40444
ID ADE40444 standard; DNA; 3707 BP.

AC ADE40444;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human receptor tyrosine kinase TRKB (gene ID 5816) DNA.

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XX      AIDS; acquired immunodeficiency syndrome; human immunodeficiency virus;
KM      HIV-related disorder; differential expression; drug screening;
KM      viral replication modulation; diagnosis; prognosis; predisposition;
KM      anti-HIV; gene therapy; antinease therapy; human;
KM      receptor tyrosine kinase TRKB; gene; de.
OS      Homo sapiens.
FH      Key Location/Qualifiers
FT      CDS 352..2820
FT      /tag= a
FT      /product= "Human receptor tyrosine kinase TRKB"
PN      WO2003070883-A2.
XX      28-AUG-2003.
XX      13-FEB-2003; 2003WO-US004246.
XX      15-FEB-2002; 2002US-0357391P.
XX      13-MAY-2002; 2002US-0380249P.
XX      25-JUN-2002; 2002US-0391306P.
XX      27-AUG-2002; 2002US-0406297P.
XX      19-SEP-2002; 2002US-0412007P.
XX      10-OCT-2002; 2002US-0417508P.
XX      10-DEC-2002; 2002US-0432318P.
PA      (MILL-) MILLENNIUM PHARM INC.
PI      Powell DM, Welch NS;
XX      WPI; 2003-671808/63.
XX      P-PSDB; ADE40445.
XX      Identifying a compound capable of diagnosing, preventing or treating AIDS
PT      or an HIV-related disorder comprises assaying the ability of the compound
PT      to modulate e.g. 1414, 1481 or 1553 nucleic acid expression or
PT      polypeptide activity.
PS      Claim 1; SEQ ID NO 23; 167bp; English.
XX      The invention relates to a method of identifying a compound useful in the
CC      treatment of AIDS (acquired immunodeficiency syndrome) or an HIV (human
CC      immunodeficiency virus)-related disorder. The invention involves assaying
CC      the ability of a test compound to modulate the activity or expression of
CC      26 human proteins. These proteins and nucleic acids encoding them
CC      (ADE40422-ADE40473) are differentially expressed in tissues relating to
CC      AIDS or an HIV-related disorder compared to their expression in normal
CC      tissues. The invention also relates to the use of the compounds
CC      identified to modulate viral replication in a cell and to treat a patient
CC      with AIDS or an HIV-related disorder. The invention further discloses
CC      methods for the diagnostic evaluation and prognosis of various HIV-
CC      related disorders, and for the identification of individuals exhibiting a
CC      predisposition to such conditions. The modulatory compounds identified
CC      using the method of the invention may be small organic molecules,
CC      peptides, antibodies or antinease nucleic acid molecules. The methods of
CC      the invention are useful in diagnosing, preventing or treating AIDS or
CC      HIV-related disorders. The present sequence represents a human
CC      polynucleotide which is differentially expressed in AIDS or HIV-related
CC      disorders.
SQ      Sequence 3707 BP; 942 A; 948 C; 900 G; 917 T; 0 U; 0 Other;
XX

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Query Match 100.0%; Score 3707; DB 10; Length 3707;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCATTCCGATCTAACAGAAATCTGCGCCGAGAGTCCCGAGCGCGCGGTCCG 60
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Db 61 TGCCGGGCGCCGGCCATGCAGCGCGCCGCGGAGCTCCGACACGGGAGGCG 120
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Db 121 CCCCTGTAAAGCGGTTCCGTATGCGGGGACCACTGTGAACCTTGGCGGCTGGCGGAACA 180
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Db 181 CTCTTCGTCCGGAACGAGCTGAGCTGTATGAGCTGGACTCGGCAACGCCGGAACAAGC 240
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Db 2221 GACCTCAACAGTTCCTCAGGGCACAGGCGCTGTATGCTGTGATGCTGAGGCAAC 2280

QY 2281 CCGGCCACGAACTGAGCAGTCCGAGATGCTGCATATAGCCCGACAGATGCGCCGGCC 2340
DB 2281 CCGGCCACGAACTGAGCAGTCCGAGATGCTGCATATAGCCCGACAGATGCGCCGGCC 2340
QY 2241 ATGGCTACCGTGGGCGCCAGCAGTTCGTGACACCGCATTTGGCCACCAAGAACTGGCTG 2400
DB 2241 ATGGCTACCGTGGGCGCCAGCAGTTCGTGACACCGCATTTGGCCACCAAGAACTGGCTG 2400
QY 2401 GTCCGGGAGAACTTGCTGTGTAAATCGGGGACTTTGGGATGTCCGGGAGGTGTACAGC 2460
DB 2401 GTCCGGGAGAACTTGCTGTGTAAATCGGGGACTTTGGGATGTCCGGGAGGTGTACAGC 2460
QY 2461 ACTGACTACTACAGGGTGTGGCCACCAATGCTGCCATTGCTGTGATGCTTCACAG 2520
DB 2461 ACTGACTACTACAGGGTGTGGCCACCAATGCTGCCATTGCTGTGATGCTTCACAG 2520
QY 2521 AGCATCATGTACAGAAATTCAGACAGGAAAGCGACTGGAGCGTGGGGGTGTGTGTG 2580
DB 2521 AGCATCATGTACAGAAATTCAGACAGGAAAGCGACTGGAGCGTGGGGGTGTGTGTG 2580
QY 2581 TGGGAGATTTTCACTATGGAACAGCCCTGTGTACAGCTGTCAAACAATGAGGTATA 2640
DB 2581 TGGGAGATTTTCACTATGGAACAGCCCTGTGTACAGCTGTCAAACAATGAGGTATA 2640
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DB 2641 GAGTGTATCACTACAGGCGCAGTCTGTGACGACCCCGCAGCGTGGCCCGAGAGGTAT 2700
QY 2701 GAGCTGATGCTGGGGGTGTGGCAGAGAGCCCGACATGAGAAAGAAATCAAGGGCATC 2760
DB 2701 GAGCTGATGCTGGGGGTGTGGCAGAGAGCCCGACATGAGAAAGAAATCAAGGGCATC 2760
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DB 2761 CATACCTCTCTTCAAGAACTTGCCCAAGGCACTCCGCTGTACTGAGCACTTGAAGCTAG 2820
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DB 2821 GGGCCCTTTTCCCGACCGATCTTCCCAAGTACTCTCCAGAGGGGTGAGAGATGAA 2880
QY 2881 CATCTTTTAATGCGCGCTGAGAGGCCAACAAGCTCTCCCTTCACTCGAAGATTTAAC 2940
DB 2881 CATCTTTTAATGCGCGCTGAGAGGCCAACAAGCTCTCCCTTCACTCGAAGATTTAAC 2940
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DB 2941 ATCAAAAGACTCCGAAAGCTCTCGAGGGAAGCAAGTGTACTTCTTCACTCATAGACAA 3000
QY 3001 GTATTTGACTTTTGGCATTAATCTCTTCTCTTCCATCTCCCTTGGTGTCTT 3060
DB 3001 GTATTTGACTTTTGGCATTAATCTCTTCTCTTCCATCTCCCTTGGTGTCTT 3060
QY 3061 TTTCTTTTAAATTTTCTTTCTTTCTTTTGTGCTTCCCTGCTTACAGATTTCTT 3120
DB 3061 TTTCTTTTAAATTTTCTTTCTTTCTTTTGTGCTTCCCTGCTTACAGATTTCTT 3120
QY 3121 ACCCTTTTGAATCAATCTGCTTGTGATTAATTAATCTGTGATGAGAAAGGC 3180
DB 3121 ACCCTTTTGAATCAATCTGCTTGTGATTAATTAATCTGTGATGAGAAAGGC 3180
QY 3181 CTTTAAACAAAGTAAATTTGTATATACAGACACTCCAGTTTGGCCACCAACTAACAA 3240
DB 3181 CTTTAAACAAAGTAAATTTGTATATACAGACACTCCAGTTTGGCCACCAACTAACAA 3240
QY 3241 TGCCTGTGTATTCCTGCTTTGATGTGATGAAAGAAAGGAAAGAAATTTTCACT 3300
DB 3241 TGCCTGTGTATTCCTGCTTTGATGTGATGAAAGAAAGGAAAGAAATTTTCACT 3300
QY 3301 TAAACTTGTCACTCTGCTGATGAGATATGAGAGTTTCTATGATTCACCTGATTTA 3360
DB 3301 TAAACTTGTCACTCTGCTGATGAGATATGAGAGTTTCTATGATTCACCTGATTTA 3360

QY 3361 TTTATTTATTAATCTGCTTATTTGTTTGTGATGCTTAAGCTGTGATTAAGAA 3420
DB 3361 TTTATTTATTAATCTGCTTATTTGTTTGTGATGCTTAAGCTGTGATTAAGAA 3420
QY 3421 AACTTGTTCATCTGTGAGGCTTTATCTATGAGAGATTTAAACAGAGAAAG 3480
DB 3421 AACTTGTTCATCTGTGAGGCTTTATCTATGAGAGATTTAAACAGAGAAAG 3480
QY 3481 ATTATTTATTAACCGCAATATGAGAGAAACAAAGACCACTGGATCAAGCTGTGTCA 3540
DB 3481 ATTATTTATTAACCGCAATATGAGAGAAACAAAGACCACTGGATCAAGCTGTGTCA 3540
QY 3541 GTCCCTAATTAGAAATACTCAGCAACTGTACTGTGGAGAAATGATTTGGCACTTCC 3600
DB 3541 GTCCCTAATTAGAAATACTCAGCAACTGTACTGTGGAGAAATGATTTGGCACTTCC 3600
QY 3601 CTTGAGGACCTTTCTGAGGAGTAAAAAGACTACTGCTGTGATGATTTCTT 3660
DB 3601 CTTGAGGACCTTTCTGAGGAGTAAAAAGACTACTGCTGTGATGATTTCTT 3660
QY 3661 TCCCATCACCAGAAATGATAGCTGTGAGAGAGCAAGATGCTT 3707
DB 3661 TCCCATCACCAGAAATGATAGCTGTGAGAGAGCAAGATGCTT 3707
RESULT 6
ADN39075
ID ADN39075 standard; cDNA; 3707 BP.
XX
AC ADN39075;
XX
DT 17-JUN-2004 (first entry)
XX
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:393.
XX
KW Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; lechemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW renal neovascularization syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiac; immunomodulatory;
KW vulnery; gene therapy; vaccine; gene; ss.
XX
OS Homo sapiens.
XX
PN W0203042661-A2.
XX
PD 22-MAY-2003.
XX
PF 13-NOV-2002; 2002WC-US036810.
XX
PR 13-NOV-2001; 2001US-0350666P.
PR 21-NOV-2001; 2001US-0332464P.
PR 29-NOV-2001; 2001US-0334393P.
PR 03-DEC-2001; 2001US-0335394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-0355250P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-0368809P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.
PR 16-JUL-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-0397784P.
PR 22-JUL-2002; 2002US-0397845P.
PR 09-SEP-2002; 2002US-0409450P.
XX
PA (BOSB-) EOS BIOTECHNOLOGY INC.
XX
FI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;

PI Mack DH, Murray R, Watson SR, Wilson KE, Ziolknik A;
XX WPI: 2003-468649/44.
DR P-PSDB; ADN39076.
XX
PT Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.
XX
PS Claim 8; SEQ ID NO 393; 1385bp; English.
XX
CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neurovascularisation syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a nucleic acid sequence of the invention.
XX
SQ Sequence 3707 BP; 942 A; 948 C; 900 G; 917 T; 0 U; 0 Other;
Query Match 100.0%; Score 3707; DB 11; Length 3707;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCCCATTCGATCTTAACAGAGATCTGCGCCCGAGAGATCCCGAGCGCCGCGTGG 60
DB 1 CCCCCATTCGATCTTAACAGAGATCTGCGCCCGAGAGATCCCGAGCGCCGCGTGG 60
QY 61 TGGCCCGGCGCCCGGCGCATGAGAGAGCGCCCGCGGAGCTCCGAGACGGGTAGCGC 120
DB 61 TGGCCCGGCGCCCGGCGCATGAGAGAGCGCCCGCGGAGCTCCGAGACGGGTAGCGC 120
QY 121 CCCCCGTAAAGCGGTTGCTATGCGCGGAGCACTGTAACTCGCGCGCTGCGGGAACA 180
DB 121 CCCCCGTAAAGCGGTTGCTATGCGCGGAGCACTGTAACTCGCGCGCTGCGGGAACA 180
QY 181 CTCTTCGCTCCGAGACAGACTGAGCTCTGTATAGCTGTGACTCGGACCGCCGCAACAGC 240
DB 181 CTCTTCGCTCCGAGACAGACTGAGCTCTGTATAGCTGTGACTCGGACCGCCGCAACAGC 240
QY 241 ACCGAGAGATTAAAGAGAGCCCGAGCGGAGAGCGCTCCCGCGACGGGTGGGGAAG 300
DB 241 ACCGAGAGATTAAAGAGAGCCCGAGCGGAGAGCGCTCCCGCGACGGGTGGGGAAG 300
QY 301 CGGCGCGTGAAGCGGAGAGAGAGCACTCGGCGTGGCACTGAGGATGTCGTC 360
DB 301 CGGCGCGTGAAGCGGAGAGAGAGCACTCGGCGTGGCACTGAGGATGTCGTC 360
QY 361 TGGATTAAGTGGAGTGAAGCCCGCATGCGCGCTCTGCGGCTTCTGCTGCTGTTTG 420
DB 361 TGGATTAAGTGGAGTGAAGCCCGCATGCGCGCTCTGCGGCTTCTGCTGCTGTTTG 420
QY 421 GGGCTTCTGAGAGGCGCTTTGGCTGTCCAGCTCTGCAAAATGAGAGCTCTCGGATC 480
DB 421 GGGCTTCTGAGAGGCGCTTTGGCTGTCCAGCTCTGCAAAATGAGAGCTCTCGGATC 480
QY 481 TGGTGAAGAGAGCCCTTCTCTGAGCATGAGGATTTCCGAGATTGAGACCTTAACGTGA 540
DB 481 TGGTGAAGAGAGCCCTTCTCTGAGCATGAGGATTTCCGAGATTGAGACCTTAACGTGA 540
QY 541 GATCTGAGAACATCAGGAATTTTCAATCGCAACAGAAAAGGTTAAGAAATCATCAAC 600
DB 541 GATCTGAGAACATCAGGAATTTTCAATCGCAACAGAAAAGGTTAAGAAATCATCAAC 600

DB 541 GATCTGAGAACATCAGGAATTTTCAATCGCAACAGAAAAGGTTAAGAAATCATCAAC 600
QY 601 GAAGATGATGTTGAAGCTTATGATGAGACTGAGAAATCTGACAAATTTGATTTGATTA 660
DB 601 GAAGATGATGTTGAAGCTTATGATGAGACTGAGAAATCTGACAAATTTGATTTGATTA 660
QY 661 AAATTTGGCTCAATTAAGCAATTTCTGAAAAAGCAACCTGACAGACATCAATTTTACC 720
DB 661 AAATTTGGCTCAATTAAGCAATTTCTGAAAAAGCAACCTGACAGACATCAATTTTACC 720
QY 721 CGAAACCAATGACAGAGTTTGTCTAGGAAACATTTCCGTCACTTGAAGTCTGAACTG 780
DB 721 CGAAACCAATGACAGAGTTTGTCTAGGAAACATTTCCGTCACTTGAAGTCTGAACTG 780
QY 781 ATTCGAGGCAATTCATTCATGAGCTCCGTGACATTAATGATGATCAAGACTCTGCA 840
DB 781 ATTCGAGGCAATTCATTCATGAGCTCCGTGACATTAATGATGATCAAGACTCTGCA 840
QY 841 GAGGCTAAATCCAGTCCAGACACTCAGGATTTGTACTGCTGAATGAAAGCAGAGAT 900
DB 841 GAGGCTAAATCCAGTCCAGACACTCAGGATTTGTACTGCTGAATGAAAGCAGAGAT 900
QY 901 ATTCCCTGCAAACTGCGAGATACCAATTTGAGTTTCCATCTGCAATCTGCGCGCA 960
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DB 1021 CCGGTTCTTAATATGATTTGGATGTTGTAACTGTGTTCAAAACATATGATGAACA 1080
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DB 1081 AGCCACACACAGGCTCTTAAAGATTACTAACATTTTCATGCAATGAGAGAGAG 1140
QY 1141 ATCTGTTGTTGGGGAAGAACTGTGAGAGAAATCAAGATTCGTCACTCACTG 1200
DB 1141 ATCTGTTGTTGGGGAAGAACTGTGAGAGAAATCAAGATTCGTCACTCACTG 1200
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QY 1441 AAGATGATGTAAGAGAGATGAGAAACAGATTTCTGCTCACTTATGAGGCTGCTGGA 1500
DB 1441 AAGATGATGTAAGAGAGATGAGAAACAGATTTCTGCTCACTTATGAGGCTGCTGGA 1500
QY 1501 ATTGACGATGATGCAAAACCCAAATTAATCTGATTAATTAATTAATTAATTAATTAAT 1560
DB 1501 ATTGACGATGATGCAAAACCCAAATTAATCTGATTAATTAATTAATTAATTAATTAAT 1560
QY 1561 GCGAATGACATCGGAGACCAACAGACAGAGATGATGAATCCCTTCCACAGAGTCACT 1620
DB 1561 GCGAATGACATCGGAGACCAACAGACAGAGATGATGAATCCCTTCCACAGAGTCACT 1620
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DB 1621 GATTAACCCGCTCGGGAACATCTCTGCTTATGCTGATGATGATGATGATGATGATG 1680

1681 GGATTTTGGCTTTGGTAAATGCTGTTCTGTTAAAGTTGGCAAGACACTCGAATTTGGC 1740
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1741 ATGAAGAGCCAGGCTCGGTTATCAGCAATGATGATGCTGCGACGCCACTGCATAC 1800
1801 ATCTCAATGGAGTAACTCCATCTTCTGGAAGGTGGCCAGATGCTGCTATTAT 1860
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1861 GGAATGACCAAGATCCCTGTGATTTGAAAATGCCAGTAACTTTGGCATACCAAGTCAG 1920
1861 GGAATGACCAAGATCCCTGTGATTTGAAAATGCCAGTAACTTTGGCATACCAAGTCAG 1920
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2221 GACCTCAACAGTTCCTCAAGGCGACAGGCGCTGATGCTGCTGATGCTGAGGCGAC 2280
2221 GACCTCAACAGTTCCTCAAGGCGACAGGCGCTGATGCTGCTGATGCTGAGGCGAC 2280
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3181 CTTAACAAAGTATTTGTTATATACAGACACACTCCAGTTTCCCAACCACTAACAA 3240
3181 CTTAACAAAGTATTTGTTATATACAGACACACTCCAGTTTCCCAACCACTAACAA 3240
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3301 TAAACTTTGACCTTGTGCTGTACAGATGAGAGTTCTATGATTTCACTTTATTTA 3360
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3601 CTTGAGGACCTTTCTGAGGAGTAAAAAGACTAGCTGAGCTGTGAGATGATTTCTTT 3660
3661 TCCCATACCAAGAAATGATAGCGTGCAGTGAAGGCAAAAGATGCTT 3707
3661 TCCCATACCAAGAAATGATAGCGTGCAGTGAAGGCAAAAGATGCTT 3707

RESULT: 7
ADN39737 standard; cDNA; 3707 BP.
XX ADN39737;
XX AC
XX DT 17-JUN-2004 (first entry)
XX

DB Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C109;
XX Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularization syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiac; immunomodulatory;
KW vulnery; gene therapy; vaccine; gene; ss.
XX Homo sapiens.
XX WO2003042661-A2.
XX 22-MAY-2003.
XX 13-NOV-2002; 2002WO-US036810.
XX 13-NOV-2001; 2001US-0350666P.
PR 21-NOV-2001; 2001US-0332464P.
PR 29-NOV-2001; 2001US-0334393P.
PR 03-DEC-2001; 2001US-0335394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-0355250P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-0368809P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.
PR 16-JUL-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-0397775P.
PR 22-JUL-2002; 2002US-0397845P.
PR 09-SEP-2002; 2002US-0409450P.
XX (BOSB-) EOS BIOTECHNOLOGY INC.
XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glyme R, Hevezi PA;
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnick A;
XX WPI; 2003-468649/44.
XX P-PSDB; ADN39954.
XX Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.
XX Claim 8; SEQ ID NO C109; 1385bp; English.
XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularization syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a nucleic acid sequence of the invention.
XX Sequence 3707 BP; 942 A; 948 C; 900 G; 917 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 3707; DB 11; Length 3707;
Best Local Similarity 100.0%; Pred. No. 0;

	Matches 3707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1	CCCCATTGCGATCTAACAAGAAATGCGCCCGCAGAGATCCCGACGCGCGGTCGG 60
Db 1	CCCCATTGCGATCTAACAAGAAATGCGCCCGCAGAGATCCCGACGCGCGGTCGG 60
Qy 61	TGCG 120
Db 61	TGCG 120
Qy 121	CCCCCTTAAAGCGGTTGCTATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
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Qy 181	CTTTGCTCG 240
Db 181	CTTTGCTCG 240
Qy 241	ACCGAGAGATTAAAGAGCGCGCAAGCGCGCAAGAGCGCTCCCGCGCGCGCG 300
Db 241	ACCGAGAGATTAAAGAGCGCGCAAGCGCGCAAGAGCGCTCCCGCGCGCGCG 300
Qy 301	CGGCG 360
Db 301	CGGCG 360
Qy 361	TGATTAAGTGGGCAATGGAACCGCGCATGCGCGCGCGCGCGCGCGCGCGCG 420
Db 361	TGATTAAGTGGGCAATGGAACCGCGCATGCGCGCGCGCGCGCGCGCGCGCG 420
Qy 421	GGCTTTCGAGGCGCGCTTTCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
Db 421	GGCTTTCGAGGCGCGCTTTCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
Qy 481	TGGTGCAGCGACCTTCTCTGCGCATGCGCGCATTTCCGAGATTGAGCTTA 540
Db 481	TGGTGCAGCGACCTTCTCTGCGCATGCGCGCATTTCCGAGATTGAGCTTA 540
Qy 541	GATCCTGAGAACATCAGCGAAATTTTCATGCGCAACGAGAAAGTTAGAAAT 600
Db 541	GATCCTGAGAACATCAGCGAAATTTTCATGCGCAACGAGAAAGTTAGAAAT 600
Qy 601	GAGATGATGTTGAAGCTTAATGCGGAGCTGAGAAATCGCAATTTGATTT 660
Db 601	GAGATGATGTTGAAGCTTAATGCGGAGCTGAGAAATCGCAATTTGATTT 660
Qy 661	AAATTTGCTGCTAAAGCAATTTCTGAAAACAGCAACCTGCAGCATCAATTT 720
Db 661	AAATTTGCTGCTAAAGCAATTTCTGAAAACAGCAACCTGCAGCATCAATTT 720
Qy 721	CGAAACAACTGAGAGATTTGCTAGAGAAACATTTCCGTCACCTTGCTGAA 780
Db 721	CGAAACAACTGAGAGATTTGCTAGAGAAACATTTCCGTCACCTTGCTGAA 780
Qy 781	ATTCGTTGCGCATTCATTTACATGCTCTGTCAGCAATTAATGAGATCAAG 840
Db 781	ATTCGTTGCGCATTCATTTACATGCTCTGTCAGCAATTAATGAGATCAAG 840
Qy 841	GAGGCTAAATTCAGTCCAGACACTCAGAGATTTGACTGCTGAATGAAGCA 900
Db 841	GAGGCTAAATTCAGTCCAGACACTCAGAGATTTGACTGCTGAATGAAGCA 900
Qy 901	ATTCGCTGCGCAACCTGCGAGATCCCAATTTGCTGCTGCAATTTGCTGCG 960
Db 901	ATTCGCTGCGCAACCTGCGAGATCCCAATTTGCTGCTGCAATTTGCTGCG 960
Qy 961	CCTAACCTCACTGAGAGAAAGTATACATTAATCTAGTGGCAGTAT 1020
Db 961	CCTAACCTCACTGAGAGAAAGTATACATTAATCTAGTGGCAGTAT 1020
Qy 1021	CCGCTTCTAATATGATTTGAGATGTTGTAACCTGCTTTCAAACATATGA 1080
Db 1021	CCGCTTCTAATATGATTTGAGATGTTGTAACCTGCTTTCAAACATATGA 1080

QY 1081 AGCCACACAGGGGCTCTTAAGATACTAACATTTTCATCCGATGACAGTGGAGAG 1140
DB 1081 AGCCACACAGGGGCTCTTAAGATACTAACATTTTCATCCGATGACAGTGGAGAGAG 1140
QY 1141 ATCTCTGTGTGGGAAAATCTTGTAGGAGAGATGAAGATTCGTGCAACTTCACGTG 1200
DB 1141 ATCTCTGTGTGGGAAAATCTTGTAGGAGAGATGAAGATTCGTGCAACTTCACGTG 1200
QY 1201 CATTTGACACCACTATCACATTTCTCGAATCTCGAACTCAGACACACTGTGTGATT 1260
DB 1201 CATTTGACACCACTATCACATTTCTCGAATCTCGAACTCAGACACACTGTGTGATT 1260
QY 1261 CCATTCACTGTGAAGGCAACCCCAACCAAGCGCTTCAGTGTGTCTATAACGGGGCAATA 1320
DB 1261 CCATTCACTGTGAAGGCAACCCCAACCAAGCGCTTCAGTGTGTCTATAACGGGGCAATA 1320
QY 1321 TTGAAATAGTCCAAATCATCTGTAATAAATAATGATTAACATGACAGAGATACAC 1380
DB 1321 TTGAAATAGTCCAAATCATCTGTAATAAATAATGATTAACATGACAGAGATACAC 1380
QY 1381 GGCTGCTCCAGCTGATTAATCCCACTCACATGAACAATGGGAGCTACACTTAATAGCC 1440
DB 1381 GGCTGCTCCAGCTGATTAATCCCACTCACATGAACAATGGGAGCTACACTTAATAGCC 1440
QY 1441 AAGAATGATATGGGAAGATGAGAAAACAGATTTCTGCTCATAGGCTGGCTTGA 1500
DB 1441 AAGAATGATATGGGAAGATGAGAAAACAGATTTCTGCTCATAGGCTGGCTTGA 1500
QY 1501 ATTGACATGGTGGAAACCCAAATTAATCCGATGATTAATTAAGAAATTAAGAACTGCA 1560
DB 1501 ATTGACATGGTGGAAACCCAAATTAATCCGATGATTAATTAAGAAATTAAGAACTGCA 1560
QY 1561 GCGAATGACATCGGGGACACCAACGAGAAGATGAATAATCCCTTCCACAGAGTCACT 1620
DB 1561 GCGAATGACATCGGGGACACCAACGAGAAGATGAATAATCCCTTCCACAGAGTCACT 1620
QY 1621 GATTAACACCGGTGGGAAACATCTTCGGTCTATGCTGTGTGTGTGTGTGTGTGTGT 1680
DB 1621 GATTAACACCGGTGGGAAACATCTTCGGTCTATGCTGTGTGTGTGTGTGTGTGTGT 1680
QY 1681 GGATTTTGGCTTTTGTATATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1740
DB 1681 GGATTTTGGCTTTTGTATATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1740
QY 1741 ATGAAGAGCCAGCTCGCTTATCAGCAATGATGATGATGATGATGATGATGATGATGAT 1800
DB 1741 ATGAAGAGCCAGCTCGCTTATCAGCAATGATGATGATGATGATGATGATGATGATGAT 1800
QY 1801 ATCTCCATGGAGTAACTCCATCTTCTCGAAGGTGGCCAGATGCTGTATATT 1860
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QY 1861 GGAATGACCAAGATCCCTGTATGAAAAATCCCAAGTATGGAATGGAATGGAATGGAAT 1920
DB 1861 GGAATGACCAAGATCCCTGTATGAAAAATCCCAAGTATGGAATGGAATGGAATGGAAT 1920
QY 1921 CTCAAGCAGACACATTTGTTCAGCACATCAAGGACATAATTTGTCTGAAAAAGGAG 1980
DB 1921 CTCAAGCAGACACATTTGTTCAGCACATCAAGGACATAATTTGTCTGAAAAAGGAG 1980
QY 1981 CTAGGCGAAGAGCCTTTGAAAAAGTGTCTAGCTGAATGTAATCTGTGTCTGTAG 2040
DB 1981 CTAGGCGAAGAGCCTTTGAAAAAGTGTCTAGCTGAATGTAATCTGTGTCTGTAG 2040
QY 2041 CAGACAAAGATCTTGT 2100
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DB 2101 GACTTCCACGCTGAGGCGAGCTCTGACCAACCTCCAGATGAGACATGCTCAAGTTC 2160

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DB 2161 TATGGGCTGCTGCTGAGAGGCGACCCCTCATCATGTCTTTAGATACATGAGCATGGG 2220
QY 2221 GACCTCAACAAAGTCTCTCAGGGGACACAGGCTGATGAGCTGTGTGTGTGTGTGTGTGT 2280
DB 2221 GACCTCAACAAAGTCTCTCAGGGGACACAGGCTGATGAGCTGTGTGTGTGTGTGTGTGT 2280
QY 2281 CCGCCACCGAATCTGACGAGTGCAGATGCTGATATAGCCAGACAGATGCGCGGGG 2340
DB 2281 CCGCCACCGAATCTGACGAGTGCAGATGCTGATATAGCCAGACAGATGCGCGGGG 2340
QY 2341 ATGCTACTGCGGCTGCCAGCATCTGTGTACACCGGATTTTGGCCACCAAGAACTGTCTG 2400
DB 2341 ATGCTACTGCGGCTGCCAGCATCTGTGTACACCGGATTTTGGCCACCAAGAACTGTCTG 2400
QY 2401 GTGCGGGAGAACTTGTGTGAAATCGGGGACTTTTGGATGTCCGGGAGGTGACAGC 2460
DB 2401 GTGCGGGAGAACTTGTGTGAAATCGGGGACTTTTGGATGTCCGGGAGGTGACAGC 2460
QY 2461 ACTGACTACTACAGGCTCGGTGGCCACACATGCTGCCATTTGCTGTGTGTGTGTGTGTGT 2520
DB 2461 ACTGACTACTACAGGCTCGGTGGCCACACATGCTGCCATTTGCTGTGTGTGTGTGTGTGT 2520
QY 2521 AGCATCATGTACAGAAATTCACAGAGGAAAGGAGCGTCTGAGAGCTGTGGGGTGTGTGTG 2580
DB 2521 AGCATCATGTACAGAAATTCACAGAGGAAAGGAGCGTCTGAGAGCTGTGGGGTGTGTGTG 2580
QY 2581 TGGGAGATTTTCACTATGGCAACAGCCCTGTGACAGCTGTCAACATGAGATGATA 2640
DB 2581 TGGGAGATTTTCACTATGGCAACAGCCCTGTGACAGCTGTCAACATGAGATGATA 2640
QY 2641 GAGTGTATCACTCAGGGCCGAGTCTGTGACGACCCCGACAGTGTGCCCGACAGAGTGTAT 2700
DB 2641 GAGTGTATCACTCAGGGCCGAGTCTGTGACGACCCCGACAGTGTGCCCGACAGAGTGTAT 2700
QY 2701 GAGCTGATGCTGGGGTGTCTGTGACGAGAGGCCCAATGAGAAACATCAAGGGATC 2760
DB 2701 GAGCTGATGCTGGGGTGTCTGTGACGAGAGGCCCAATGAGAAACATCAAGGGATC 2760
QY 2761 CATACCTCTCTTACAGAACTTGGCAAGGACATCTCCGGTCTACCTGTACATTTAGGCTAG 2820
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DB 2881 CATCTTTTAACTGCGCTGAGAGCCACCAAGCTGTCTCTTCACTGTGACATTTAAC 2940
QY 2941 ATCAAGACCTCGAGAACTCTGAGGGGAGAGTGTGTACTTTCATCATAGACACA 3000
DB 2941 ATCAAGACCTCGAGAACTCTGAGGGGAGAGTGTGTACTTTCATCATAGACACA 3000
QY 3001 GATATGACTCTTTTGGCATTAATCTTCTCTCTTCCATCTGCCCTGTGTGTCTT 3060
DB 3001 GATATGACTCTTTTGGCATTAATCTTCTCTCTTCCATCTGCCCTGTGTGTCTT 3060
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DB 3061 TTTCTTTTAAATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 3120
QY 3121 ACCCTTCTTGAATCAATGCGCTTGTGATTAATTAATCTGATGACATGACAAAGGC 3180
DB 3121 ACCCTTCTTGAATCAATGCGCTTGTGATTAATTAATCTGATGACATGACAAAGGC 3180
QY 3181 CTTAACAAAGTATTTGTTATATACAGACACACTCCAGTTTGGCCACCACTAACAA 3240
DB 3181 CTTAACAAAGTATTTGTTATATACAGACACACTCCAGTTTGGCCACCACTAACAA 3240
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Db 3241 TGCCTGTGTATTCCTGCTTGTATGTGATGAAAAAGGAAAAAANAATATTTCACT 3300
 Qy 3301 TAAACTTTGCACTTGTGCTGTACAGATATGAGAGATTTCTATGATTTCACTTATTTA 3360
 Db 3301 TAAACTTTGCACTTGTGCTGTACAGATATGAGAGATTTCTATGATTTCACTTATTTA 3360
 Qy 3361 TTTATTTATTTACTGTTCTTATTTGTTTTGGATGGCTTAAAGCTGTGTATTTAAAAAGAA 3420
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 Qy 3421 AACTTGTGTCAATCTGTGAAGCTTTATCTATGAGATTTAAACCAAGAGAAAAAGAG 3480
 Db 3421 AACTTGTGTCAATCTGTGAAGCTTTATCTATGAGATTTAAACCAAGAGAAAAAGAG 3480
 Qy 3481 ATTATTTATGAACCGCAATATGAGAGAACCAAGACCACTGGATCAGCTGTGTCA 3540
 Db 3481 ATTATTTATGAACCGCAATATGAGAGAACCAAGACCACTGGATCAGCTGTGTCA 3540
 Qy 3541 GTCCCTACTTAGAATACTCAGCACTGTTAGCTGGAGAAATGTATTCGGCACTTCC 3600
 Db 3541 GTCCCTACTTAGAATACTCAGCACTGTTAGCTGGAGAAATGTATTCGGCACTTCC 3600
 Qy 3601 CCTGAGACCTTTCTGAGAGATTAAGAAAGACTAGCTGCTCTGTGCCATGATGATTCCTT 3660
 Db 3601 CCTGAGACCTTTCTGAGAGATTAAGAAAGACTAGCTGCTCTGTGCCATGATGATTCCTT 3660
 Qy 3661 TCCCATACACGAATAATGATGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3707
 Db 3661 TCCCATACACGAATAATGATGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3707

RESULT 8
ABX76428

ID ABX76428 standard; DNA; 4057 BP.

XX AC ABX76428;

XX DT 02-APR-2003 (first entry)

XX DE Lung cancer-associated polynucleotide #292.

XX KM Lung cancer-associated polynucleotide; gene; ds; cytosolic; emphysema;
 KM antiinflammatory; antisthmatic; non-small cell lung cancer; atelectasis;
 KM small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KM chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KM interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
 XX OS Unidentified.
 XX PN WO200286443-A2.
 XX PD 31-OCT-2002.
 XX PF 18-APR-2002; 2002WO-US012476.
 XX PR 18-APR-2001; 2001US-0284477P.
 PR 10-MAY-2001; 2001US-0280492P.
 PR 09-NOV-2001; 2001US-0339245P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 29-NOV-2001; 2001US-0334370P.
 PR 12-APR-2002; 2002US-0372246P.
 XX PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX PT Aziz N, Murray R;
 XX WI: 2003-093161/08.
 DR P-PSDB; ABUS6699.
 XX

PT Detecting a lung cancer-associated transcript in a cell from a patient
 PT for treating lung cancer, by contacting a biological sample from the
 PT patient with a polynucleotide that exhibits increased or decreased

PT expression in lung cancer.
 XX
 XX Claim 22, Page 418; 453pp; English.
 XX
 CC The invention relates to a method for detecting a lung cancer-associated
 CC transcript in a cell from a patient, comprising contacting a biological
 CC sample from the patient with a polynucleotide that selectively hybridises
 CC to a sequence that is at least 80 % identical to a gene that exhibits
 CC increased or decreased expression in lung cancer samples. Lung cancer-
 CC associated polynucleotides and polypeptides are used for identifying a
 CC compound that modulates a lung cancer-associated polypeptide, for
 CC inhibiting proliferation of a lung cancer-associated cell to treat lung
 CC cancer in a patient and for treating a mammal having lung cancer by
 CC administering a modulatory compound identified. The methods are useful
 CC for treating lung cancer, such as small cell lung cancer, non-small cell
 CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
 CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
 CC hypersecretivity pneumonitis, interstitial pulmonary fibrosis, asthma and
 CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
 CC for diagnostic purposes and as targets for screening for therapeutic
 CC compounds that modulate lung cancer, such as antibodies. Sequences
 CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
 CC invention
 XX
 XX Sequence 4057 BP; 1013 A; 1033 C; 1014 G; 997 T; 0 U; 0 Other;
 XX
 SQ
 Query Match 98.4%; Score 3649; DB 8; Length 4057;
 Best Local Similarity 98.7%; Pred. No. 0;
 Matches 3707; Conservative 0; Mismatches 0; Indels 48; Gaps 1;
 Qy 1 CCCCATTGCGATCTTAACAAGAAATCTGCGCCCGAGAGTCCCGACGCCGCCGCTCGG 60
 Db 132 CCCCATTGCGATCTTAACAAGAAATCTGCGCCCGAGAGTCCCGACGCCGCCGCTCGG 191
 Qy 61 TGCCTGCG 120
 Db 192 TGCCTGCG 251
 Qy 121 CCCCCTGTAAGCGGTTGCGTATGCGCGGACCACTGTGAACCTTGCSCGCTGCCGGAACA 180
 Db 252 CCCCCTGTAAGCGGTTGCGTATGCGCGGACCACTGTGAACCTTGCSCGCTGCCGGAACA 311
 Qy 181 CTTTCTGCTCCGACCGACTCAAGCTCTGTAAAGCTGTAAGTCTGCGACGCCCGCAACAAGC 240
 Db 312 CTTTCTGCTCCGACCGACTCAAGCTCTGTAAAGTCTGTAAGTCTGCGACGCCCGCAACAAGC 371
 Qy 241 ACCGAGAGTTTAAAGAGCGCGCAAGCGCGCAAGAGGCTTCCCGCACGGGTGGGGAAG 300
 Db 372 ACCGAGAGTTTAAAGAGCGCGCAAGCGCGCAAGAGGCTTCCCGCACGGGTGGGGAAG 431
 Qy 301 CGGCGGTTGACGCGCGGGAACAGCACTCGGGCTGCGAATGCTGATGAGATTCGCTCC 360
 Db 432 CGGCGGTTGACGCGCGGGAACAGCACTCGGGCTGCGAATGCTGATGAGATTCGCTCC 491
 Qy 361 TGGATAAGTGGACATGACCGCGCATGCGCGCTGCGGGCTTCTGCTGGCTGTTGTG 420
 Db 492 TGGATAAGTGGACATGACCGCGCATGCGCGCTGCGGGCTTCTGCTGGCTGTTGTG 551
 Qy 421 GGGCTTGAAGGGCGGCTTTCGCTGTCACAGTCTCTGCAATGACATGCTCTCGATC 480
 Db 552 GGGCTTGAAGGGCGGCTTTCGCTGTCACAGTCTCTGCAATGACATGCTCTCGATC 611
 Qy 481 TGGTGAAGCAACCTTCTCTGGAATGCGATTCCTCGAATGAGAGCTTAAGAGTGA 540
 Db 612 TGGTGAAGCAACCTTCTCTGGAATGCGATTCCTCGAATGAGAGCTTAAGAGTGA 671
 Qy 541 GATCTGAGAAATCAACGAAATTTTTCATGCAAAACGAAAGAGTTGAAATCATCAAC 600
 Db 672 GATCTGAGAAATCAACGAAATTTTTCATGCAAAACGAAAGAGTTGAAATCATCAAC 731
 Qy 601 GAAGATGATGTTGAAGTTATGTTGAGCTGAGAAATCTGCAATTTGATTTCTGATTTA 660
 Db 732 GAAGATGATGTTGAAGTTATGTTGAGCTGAGAAATCTGCAATTTGATTTCTGATTTA 791

QY 661 AAATTGTGGCTCATTAAGCATTTCTGAAAAACGCAACCTGCGACGACATCATTTTACC 720
DB 792 AAATTGTGGCTCATTAAGCATTTCTGAAAAACGCAACCTGCGACGACATCATTTTACC 851
QY 721 CGAAACAAACGACGAGTTTGTCTAGAGAAACATTTCCGTCACTGACCTTGCTGTGAACTG 780
DB 852 CGAAACAAACGACGAGTTTGTCTAGAGAAACATTTCCGTCACTGACCTTGCTGTGAACTG 911
QY 781 ATCTGTGTGGGCAATCCATTTTACATGCTCTGTGACATTTATGTGGATCAAGAATCTTCCA 840
DB 912 ATCTGTGTGGGCAATCCATTTTACATGCTCTGTGACATTTATGTGGATCAAGAATCTTCCA 971
QY 841 GAGGCTAAATCCAGTCCAGACATCTCAGATTTTGTACTGCTGAAATGAAGACGAGAAT 900
DB 972 GAGGCTAAATCCAGTCCAGACATCTCAGATTTTGTACTGCTGAAATGAAGACGAGAAT 1031
QY 901 ATTCCCTGGCAAACTGCGAGATACCAATTTGTGGTTTGGCATGTGCAAAATCTGGCCGCA 960
DB 1032 ATTCCCTGGCAAACTGCGAGATACCAATTTGTGGTTTGGCATGTGCAAAATCTGGCCGCA 1091
QY 961 CCTAACCTCATGTGAGAGAGAAAGTCTATCATTAATCTGTAGTGTGCGAGGTAT 1020
DB 1092 CCTAACCTCATGTGAGAGAGAAAGTCTATCATTAATCTGTAGTGTGCGAGGTAT 1151
QY 1021 CCGGTTCTTAATATGTATTTGGAGTGTGGTAACTGTGTTCCAAACATATGAATGAACA 1080
DB 1152 CCGGTTCTTAATATGTATTTGGAGTGTGGTAACTGTGTTCCAAACATATGAATGAACA 1211
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DB 1212 AGGCACACAGAGGCTCTTAAGGATTAACCTTAACCTTCACCGATGACATGGGGAAGCAG 1271
QY 1141 ATCTGTGTGTGGCGGAAAACTTTGTAGAGAGATCAAGATTTCTGTCAACCTCACTGTG 1200
DB 1272 ATCTGTGTGTGGCGGAAAACTTTGTAGAGAGATCAAGATTTCTGTCAACCTCACTGTG 1331
QY 1201 CATTTTGACCACTATATCATTTTCTGAAATCTGCAACCTGACGACCACTGTGCAAT 1260
DB 1332 CATTTTGACCACTATATCATTTTCTGAAATCTGCAACCTGACGACCACTGTGCAAT 1391
QY 1261 CCAATTCAGTGAAGGCAACCCCAACCAAGCGCTTCAAGTGTCTTAACGGGGCAATA 1320
DB 1392 CCAATTCAGTGAAGGCAACCCCAACCAAGCGCTTCAAGTGTCTTAACGGGGCAATA 1451
QY 1321 TTGAATGAGTCCAATATCATCTGTACTAAATATACATGTACCAATCAACGAGATACAC 1380
DB 1452 TTGAATGAGTCCAATATCATCTGTACTAAATATACATGTACCAATCAACGAGATACAC 1511
QY 1381 GGCTGCTCCAGCTGGAATATCCCATGACATGAACAATGGGGACTACCTTAATAGCC 1440
DB 1512 GGCTGCTCCAGCTGGAATATCCCATGACATGAACAATGGGGACTACCTTAATAGCC 1571
QY 1441 AAGAAATAGTATGGGAGAGATGAGAAACAGATTTCTGCTCACTTCAAGGCTGCTGGA 1500
DB 1572 AAGAAATAGTATGGGAGAGATGAGAAACAGATTTCTGCTCACTTCAAGGCTGCTGGA 1631
QY 1501 ATTGACATGATGCAAAACCAAAATTTATCTGATGTAATTTATGAAGATTAATGAACCTGA 1560
DB 1632 ATTGACATGATGCAAAACCAAAATTTATCTGATGTAATTTATGAAGATTAATGAACCTGA 1691
QY 1561 GCGAATGACATCGGGAACCAACGACAGACAGAAATGAATGAATCCCTTTCACAGAGCTGCT 1620
DB 1692 GCGAATGACATCGGGAACCAACGACAGACAGAAATGAATGAATCCCTTTCACAGAGCTGCT 1751
QY 1621 GATTAACACCGGTGCGGAAACATCTCTCGGTCTAATGCTGTGTGTGTGTGTGTGTGTGTG 1680
DB 1752 GATTAACACCGGTGCGGAAACATCTCTCGGTCTAATGCTGTGTGTGTGTGTGTGTGTGTG 1811
QY 1681 GGAATTTGCTTTTGTATGCTGTCTGTGTAAGTTGGCAGACACTCAAGTTTGGC 1740
DB 1812 GGAATTTGCTTTTGTATGCTGTCTGTGTAAGTTGGCAGACACTCAAGTTTGGC 1871

QY 1741 ATGAAA-----GGCCCA 1752
DB 1872 ATGAAAATTTTCATGTTTGGATTTGGAAAATGAATCAAGACAGGTGTTGGCCCA 1931
QY 1753 GCCTCCGTTATCAGCAATGATGATGACTCTGCGAGGCCACTCCATGCATCTCCAAATGGG 1812
DB 1932 GCCTCCGTTATCAGCAATGATGATGACTCTGCGAGGCCACTCCATGCATCTCCAAATGGG 1991
QY 1813 AGTAACATTCATCTTCTTGGAAGGTGGCCAGATGCTGTCTAATTTGGAATGACCAAG 1872
DB 1992 AGTAACATTCATCTTCTTGGAAGGTGGCCAGATGCTGTCTAATTTGGAATGACCAAG 2051
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DB 2052 ATCCCTGATATGAAAATCCCGATACCTTTGGATACCAACAGTCAAGCTCAAGCCAGAC 2111
QY 1933 ACATTTGTTCAAGCATATCAAGCGACATTAACATTTGTTCTGAAAAGGAGCTAAGCGAAGGA 1992
DB 2112 ACATTTGTTCAAGCATATCAAGCGACATTAACATTTGTTCTGAAAAGGAGCTAAGCGAAGGA 2171
QY 1993 GCCTTTGAAAAGTGTCTTGTAGTGAATGCTAATACCTGTGCTGAGCAGACAAAGATC 2052
DB 2172 GCCTTTGAAAAGTGTCTTGTAGTGAATGCTAATACCTGTGCTGAGCAGACAAAGATC 2231
QY 2053 TTGTGTGCAGTGAAGACCTCGAAGAGATGCCAGTGAACATGACGCAAGGACCTTCCACCT 2112
DB 2232 TTGTGTGCAGTGAAGACCTCGAAGAGATGCCAGTGAACATGACGCAAGGACCTTCCACCT 2291
QY 2113 GAGGCGAGCTCTGACCAACCTCCAGCATGAGCAGCATGCTCAAGTTCTATGAGGCTGTG 2172
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QY 2173 GTGAGGCGAGCCCTCATCATGCTCTTTGAGTACATGAAGCATGAGGAGCCTCAACAG 2232
DB 2352 GTGAGGCGAGCCCTCATCATGCTCTTTGAGTACATGAAGCATGAGGAGCCTCAACAG 2411
QY 2233 TTGCTGAGGCAACAGGCTCTGATGCGCTGTGTATGCTGAGGAGCAACCGGCCAAGGAA 2292
DB 2412 TTGCTGAGGCAACAGGCTCTGATGCGCTGTGTATGCTGAGGAGCAACCGGCCAAGGAA 2471
QY 2293 CTGACGAGTGGAGATGCTGATATAGCCAGCAGATGCGCGGGGCAATGATCTACCTG 2352
DB 2472 CTGACGAGTGGAGATGCTGATATAGCCAGCAGATGCGCGGGGCAATGATGATCTACCTG 2531
QY 2353 GCGTCCAGACCTTGTGCAACCGGATTTGGCCACAGAACTGCTGTGTGGGAGAAC 2412
DB 2532 GCGTCCAGACCTTGTGCAACCGGATTTGGCCACAGAACTGCTGTGTGGGAGAAC 2591
QY 2413 TTGCTGTGAAAATCGGGGACTTTGGGATGTCCCGGAGCGTGTACAGCATGACTACTAC 2472
DB 2592 TTGCTGTGAAAATCGGGGACTTTGGGATGTCCCGGAGCGTGTACAGCATGACTACTAC 2651
QY 2473 AGGATGGTGGCCACAAATGCTGCCCATTCGCTGATGCTCAGAGAGCATCATGTAC 2532
DB 2652 AGGATGGTGGCCACAAATGCTGCCCATTCGCTGATGCTCAGAGAGCATCATGTAC 2711
QY 2533 AGGAAATTCACGACGAAAAGCGAGCTCTGAGAGCTGGGAGTCCGTGTGTGGAGATTTTC 2592
DB 2712 AGGAAATTCACGACGAAAAGCGAGCTCTGAGAGCTGGGAGTCCGTGTGTGGAGATTTTC 2771
QY 2593 ACCTATGGCAACAGCCCTGTGTACAGAGCTGTCAACATATGAGGTATATGATATCAT 2652
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QY 2713 GGGTGTGCGAGCGAAGGCCCAATGAGGAAGAAATCAAGAGGATTCATACCTCTCT 2772
DB 2892 GGGTGTGCGAGCGAAGGCCCAATGAGGAAGAAATCAAGAGGATTCATACCTCTCT 2951
QY 2773 CAGAACTTGCCAAAGGATCTCGGTCTACCTGGAATTTCTAGGCTTAGGGCCCTTTTCCC 2832

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Qy      ||| 2833 CAGACCGATCTCTCCCAAGTACTCTCAGACGGGCTGAGAGATGAACATCTTTTAAT 2892
Db      ||| 3012 CAGACCGATCTCTCCCAAGTACTCTCAGACGGGCTGAGAGATGAACATCTTTTAAT 3071
Qy      ||| 2893 GCCGCTGAGGCGCAACAGCTGCTCTCCTTCACTTGAAGATTTACATCAAGACTCC 2952
Db      ||| 3072 GCCGCTGAGGCGCAACAGCTGCTCTCCTTCACTTGAAGATTTACATCAAGACTCC 3131
Qy      ||| 2953 GAGAACTCTGAGGGAAGCAGTGTGTACTTCTTATCATAGACAGATTTGACTCT 3012
Db      ||| 3132 GAGAACTCTGAGGGAAGCAGTGTGTACTTCTTATCATAGACAGATTTGACTCT 3191
Qy      ||| 3013 TTTGGCATPACTCTTCTGCTTTGCATCCCTGGTGGTGGCTTTCTTTTCTTTT 3072
Db      ||| 3192 TTTGGCATPACTCTTCTGCTTTGCATCCCTGGTGGTGGCTTTCTTTTCTTTT 3251
Qy      ||| 3073 AATTTCTTTTCTTTCTTTTCTTTCTGCTCTGCTCTGCTCTTACGATTTTCTTTT 3132
Db      ||| 3252 AATTTCTTTTCTTTCTTTTCTTTCTGCTCTGCTCTTACGATTTTCTTTTCTTTT 3311
Qy      ||| 3133 GAATCAATCTGCTCTTGCATTTACTTTACTTGCATAGACAAAGGCTTTAACAACT 3192
Db      ||| 3312 GAATCAATCTGCTCTTGCATTTACTTTACTTGCATAGACAAAGGCTTTAACAACT 3371
Qy      ||| 3193 AATTTGTATATACAGACAGACTCCAGTTGGCCAGCAACTAACATAGCTTTGTGTA 3252
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Qy      ||| 3253 TTCTGCTCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3312
Db      ||| 3432 TTCTGCTCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3491
Qy      ||| 3313 CTCTGCTGTAAGATATGAGAGTTTCTATGATTTCACTTCTATTTATTTATTTAT 3372
Db      ||| 3492 CTCTGCTGTAAGATATGAGAGTTTCTATGATTTCACTTCTATTTATTTATTTAT 3551
Qy      ||| 3373 ACTGCTCTTATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3432
Db      ||| 3552 ACTGCTCTTATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3611
Qy      ||| 3433 ATCTGTGAAGCCTTTATCTATGAGGATTTAAACAGAGAGAAAGATTTATTTATGA 3492
Db      ||| 3612 ATCTGTGAAGCCTTTATCTATGAGGATTTAAACAGAGAGAAAGATTTATTTATGA 3671
Qy      ||| 3493 CCGCAATATGAGGAGAAACAAAGCAACCACTGGATCAGTGTGTCAGTCCCTTAG 3552
Db      ||| 3672 CCGCAATATGAGGAGAAACAAAGCAACCACTGGATCAGTGTGTCAGTCCCTTAG 3731
Qy      ||| 3553 GAAATATCTCAGCACTGTTAGCTGGAGAAATGTTTGGGCACTTCCCTGAGAGACT 3612
Db      ||| 3732 GAAATATCTCAGCACTGTTAGCTGGAGAAATGTTTGGGCACTTCCCTGAGAGACT 3791
Qy      ||| 3613 TCTGAGAGTAAAGAAAGTAACTAGGCTCTGTGCGCATGATGATTTTCTTCCATCA 3672
Db      ||| 3792 TCTGAGAGTAAAGAAAGTAACTAGGCTCTGTGCGCATGATGATTTTCTTCCATCA 3851
Qy      ||| 3673 AAATGATATGCGTGCAGTAGAGAGCAAAAGATGCTT 3707
Db      ||| 3852 AAATGATATGCGTGCAGTAGAGAGCAAAAGATGCTT 3886

```

RESULT 9
ADN39077
ID ADN39077 standard; cDNA; 4057 BP.

ADN39077;
17-JUN-2004 (first entry)
Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:395.

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XX      ||| Human, differential expression; cancer; angiogenic disorder;
KW      ||| fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW      ||| inflammatory disease; autoimmune disease;
KW      ||| retinal neovascularisation syndrome; scarring; uterine fibroid;
KW      ||| detection; diagnosis; prognosis; drug screening; drug targeting;
KW      ||| wound healing; contraception; cytostatic; cardiac; immunomodulatory;
XX      ||| vulnery; gene therapy; vaccine; gene; ss.
XX      ||| Homo sapiens.
XX      ||| WO2003042661-A2.
XX      ||| 22-MAY-2003.
XX      ||| 13-NOV-2002; 2002WO-US036810.
XX      ||| 13-NOV-2001; 2001US-0350666P.
XX      ||| 21-NOV-2001; 2001US-032464P.
XX      ||| 29-NOV-2001; 2001US-034393P.
XX      ||| 03-DEC-2001; 2001US-035394P.
XX      ||| 14-DEC-2001; 2001US-0340376P.
XX      ||| 08-JAN-2002; 2002US-0347211P.
XX      ||| 10-JAN-2002; 2002US-0347349P.
XX      ||| 08-FEB-2002; 2002US-0355250P.
XX      ||| 13-FEB-2002; 2002US-0356714P.
XX      ||| 20-FEB-2002; 2002US-0359077P.
XX      ||| 29-MAR-2002; 2002US-0368809P.
XX      ||| 04-APR-2002; 2002US-0370110P.
XX      ||| 12-APR-2002; 2002US-037246P.
XX      ||| 05-JUN-2002; 2002US-038614P.
XX      ||| 16-JUN-2002; 2002US-0396839P.
XX      ||| 22-JUN-2002; 2002US-0397775P.
XX      ||| 22-JUN-2002; 2002US-0397845P.
XX      ||| 09-SEP-2002; 2002US-0409450P.
XX      ||| (BOSB-) BOS BIOTECHNOLOGY INC.
XX      ||| Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;
XX      ||| Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX      ||| WPI; 2003-468649/44.
XX      ||| P-PSDB; ADN39078.
XX      ||| Determining the presence or absence of a pathological cell in a patient,
XX      ||| useful for diagnosing, prognosing or treating cancer, comprises detecting
XX      ||| a nucleic acid in a biological sample.
XX      ||| Claim 8; SEQ ID NO 395; 1385bp; English.
XX      ||| The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
XX      ||| whose expression is upregulated or downregulated in specific cancers or
XX      ||| other diseases such as angiogenic or fibrotic disorders, and to methods
XX      ||| of determining the presence or absence of a pathological cell in a
XX      ||| patient by detecting a nucleic acid at least 80% identical to those of
XX      ||| the invention or by detecting a polypeptide of the invention. The
XX      ||| invention also relates to expression vectors and host cells comprising a
XX      ||| nucleic acid of the invention; antibodies which specifically bind a
XX      ||| polypeptide of the invention; use of such antibodies for drug targeting;
XX      ||| and methods of screening for modulators of activity or expression of the
XX      ||| polypeptides and nucleic acids. The nucleic acids, polypeptides,
XX      ||| antibodies and methods are useful for diagnosing, prognosing and treating
XX      ||| cancer and other conditions such as psoriasis, ischaemia, heart disease,
XX      ||| atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
XX      ||| neovascularisation syndromes, scarring and uterine fibroids. They may
XX      ||| also be useful in wound healing and in contraception. The present
XX      ||| sequence represents a nucleic acid sequence of the invention.
XX      ||| Sequence 4057 BP; 1013 A; 1033 C; 1014 G; 997 T; 0 U; 0 Other;

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Query Match 98.4%; Score 3649; DB 11; Length 4057;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 3707; Conservative 0; Mismatches 0; Indels 48; Gaps 1;

QY 1 CCCCCATTCGATCTTAACAAGGAATCTGCGCCCAAGAGTCCCGGACGCCGCCGCTCGG 60
Db 132 CCCCCATTCGATCTTAACAAGGAATCTGCGCCCAAGAGTCCCGGACGCCGCCGCTCGG 191
QY 61 TGCCCGGCGCGCGCGCATGACAGCAAGCGCGCGCGAGCTCCGAGCAGCGGTAGCGC 120
Db 192 TGCCCGGCGCGCGCGCATGACAGCAAGCGCGCGCGAGCTCCGAGCAGCGGTAGCGC 251
QY 121 CCCCCTGTAAAGCGGTTCCGTATGCGGAGCACTGTGAACCTGCGCGCTCGCGAACA 180
Db 252 CCCCCTGTAAAGCGGTTCCGTATGCGGAGCACTGTGAACCTGCGCGCTCGCGAACA 311
QY 181 CTCTTCGCTCCGAGCAAGCTCAAGCTCTGATTAAGCTGGACTCGGCAAGCCCGCAAGC 240
Db 312 CTCTTCGCTCCGAGCAAGCTCAAGCTCTGATTAAGCTGGACTCGGCAAGCCCGCAAGC 371
QY 241 ACCGAGGATTAAGAGAGCGGCAAGCGAGGAAAGGCTCCCGCAAGGCGGAGGAAAG 300
Db 372 ACCGAGGATTAAGAGAGCGGCAAGCGAGGAAAGGCTCCCGCAAGGCGGAGGAAAG 431
QY 301 CGGCGGCTGCAAGCGGAGCAAGGCACTCGGCTGGAAGCTGCTAGAGGATGCTGCC 360
Db 432 CGGCGGCTGCAAGCGGAGCAAGGCACTCGGCTGGAAGCTGCTAGAGGATGCTGCC 491
QY 361 TGAATTAAGTGGATGGAACCGGCAATGCGCGGCTCTGCGGCTTCTGCTGCTGTTGG 420
Db 492 TGAATTAAGTGGATGGAACCGGCAATGCGCGGCTCTGCGGCTTCTGCTGCTGTTGG 551
QY 421 GGCCTTCGAGAGGCGGCTTTCGCTGCTCCAGCTGCTGCAAAATGCAATGCTCTCGGATC 480
Db 552 GGCCTTCGAGAGGCGGCTTTCGCTGCTCCAGCTGCTGCAAAATGCAATGCTCTCGGATC 611
QY 481 TGGTGACGCAACCTTCTCTCGCATGCTGCAATTCGAGATTCGAGCTTACAGTGA 540
Db 612 TGGTGACGCAACCTTCTCTCGCATGCTGCAATTCGAGATTCGAGCTTACAGTGA 671
QY 541 GATCTCGAAGCAATCAACCGAAATTTTCAATGCAAAACGAAAGGTTAGAAATCATCAAC 600
Db 672 GATCTCGAAGCAATCAACCGAAATTTTCAATGCAAAACGAAAGGTTAGAAATCATCAAC 731
QY 601 GAAGATGATGTGAAGCTTAATGTGGGACTGGAATCTGCAATTTGATGATTCGATTA 660
Db 732 GAAGATGATGTGAAGCTTAATGTGGGACTGGAATCTGCAATTTGATGATTCGATTA 791
QY 661 AAATTTGTGCTCAATAAGCATTTCTGAAAAACAGCACTGACGACATCAATTTTACC 720
Db 792 AAATTTGTGCTCAATAAGCATTTCTGAAAAACAGCACTGACGACATCAATTTTACC 851
QY 721 CGAAACAACTGACGAGTTGTCTAGAAACAATTCGCTCACTTGAACCTGTGAACTG 780
Db 852 CGAAACAACTGACGAGTTGTCTAGAAACAATTCGCTCACTTGAACCTGTGAACTG 911
QY 781 ATCTGAGTGGGCAATTCATTTACATGCTCCGAGCACTTAATGTGGATCAAGACTCTCAA 840
Db 912 ATCTGAGTGGGCAATTCATTTACATGCTCCGAGCACTTAATGTGGATCAAGACTCTCAA 971
QY 841 GAGGCTAAATCACTGACGACACTCAGGATTTGTACTGCTGATGAAAGAGCAAGAAAT 900
Db 972 GAGGCTAAATCACTGACGACACTCAGGATTTGTACTGCTGATGAAAGAGCAAGAAAT 1031
QY 901 ATTCCCTGCGCAAACTGACAGATACCAATTTGTGTTTGCATCTGCAAAATCTGCGCGCA 960
Db 1032 ATTCCCTGCGCAAACTGACAGATACCAATTTGTGTTTGCATCTGCAAAATCTGCGCGCA 1091
QY 961 CCTTAACCTCACTGAGGAGAAAGGATCTATCACTTATCTGTAGTGGAGGAT 1020
Db 1092 CCTTAACCTCACTGAGGAGAAAGGATCTATCACTTATCTGTAGTGGAGGAT 1151
QY 1021 CCGGTTCTTAATATGATGAGGATGTTGGTAACTGGTTTCAAAACATGAAATGAACA 1080
Db 1152 CCGGTTCTTAATATGATGAGGATGTTGGTAACTGGTTTCAAAACATGAAATGAACA 1211

QY 1081 AGCCACACACAGGGCTTCCTTAAGATTAACATACTTCAATCCGATGACAGTGGGAAGCAG 1140
Db 1212 AGCCACACACAGGGCTTCCTTAAGATTAACATACTTCAATCCGATGACAGTGGGAAGCAG 1271
QY 1141 ATCTCTGTGTGGCGGAAAAATCTTGTAGGAAGATCAAGAATCTGTCAACCTCACTGTG 1200
Db 1272 ATCTCTGTGTGGCGGAAAAATCTTGTAGGAAGATCAAGAATCTGTCAACCTCACTGTG 1331
QY 1201 CATTTTGACCAACATACATCAATTTCTGAAATCTCAACCTCAAGACCAACTGCTGAT 1260
Db 1332 CATTTTGACCAACATACATCAATTTCTGAAATCTCAACCTCAAGACCAACTGCTGAT 1391
QY 1261 CCAATTAAGTGAAGGCAACCCCAACCGGCTTCAAGTGTCTTAATACGGGGCAATA 1320
Db 1392 CCAATTAAGTGAAGGCAACCCCAACCGGCTTCAAGTGTCTTAATACGGGGCAATA 1451
QY 1321 TTGAATGAGTCCAAATACATCTGATCAATAATACATGTTACCAATCAACGAGATACAC 1380
Db 1452 TTGAATGAGTCCAAATACATCTGATCAATAATACATGTTACCAATCAACGAGATACAC 1511
QY 1381 GGCCTGCTCCAGCTGATTAATCCCACTCAATGAACAAATGGAGACTACATTAATAGCC 1440
Db 1512 GGCCTGCTCCAGCTGATTAATCCCACTCAATGAACAAATGGAGACTACATTAATAGCC 1571
QY 1441 AAGAATGAGTGAAGGAGTGAAGAAACAGATTTCTGCTCACTTCAATGGGCTGGCTGGA 1500
Db 1572 AAGAATGAGTGAAGGAGTGAAGAAACAGATTTCTGCTCACTTCAATGGGCTGGCTGGA 1631
QY 1501 ATTGACGATGATGCAAAACCCAAATTAATCTGATGATTAATTAAGAAATTAAGAACTGCA 1560
Db 1632 ATTGACGATGATGCAAAACCCAAATTAATCTGATGATTAATTAAGAAATTAAGAACTGCA 1691
QY 1561 GCGAATGACATCGGGGACACACAGAAACAGAAATGAAGAAATCCCTTCCACAGAGTCACT 1620
Db 1692 GCGAATGACATCGGGGACACACAGAAACAGAAATGAAGAAATCCCTTCCACAGAGTCACT 1751
QY 1621 GATPAAACCGGTGCGGAAACATCTCTGAGTATAGCTGTGTGATGCTGTGCTGTG 1680
Db 1752 GATPAAACCGGTGCGGAAACATCTCTGAGTATAGCTGTGTGATGCTGTGCTGTG 1811
QY 1681 GGAATTTGCTTTGTAATGCTGTTTCTGCTTAAGTGGCAAGACCTCAAGTTTGGC 1740
Db 1812 GGAATTTGCTTTGTAATGCTGTTTCTGCTTAAGTGGCAAGACCTCAAGTTTGGC 1871
QY 1741 ATGAAA-----GGCCCA 1752
Db 1872 ATGAAAATTTTTCATGTTTGAATTTGGAAAGTAAATCAAGACAAGGTGTTGGCCA 1931
QY 1753 GCTCCGTTATCAAGCAATGATGATGACTCTGCAAGCCCACTCAATCAATCTCAATGGG 1812
Db 1932 GCTCCGTTATCAAGCAATGATGATGACTCTGCAAGCCCACTCAATCAATCTCAATGGG 1991
QY 1813 AGTAACTCCCATCTTCTTGGAAAGTGGCCAGATGCTGCTAATTTGGAATGAACCAAG 1872
Db 1992 AGTAACTCCCATCTTCTTGGAAAGTGGCCAGATGCTGCTAATTTGGAATGAACCAAG 2051
QY 1873 ATCCCTGTCAATTAATAATCCCACTTCTTGGATCAACCAAGTCAAGCTCAAGCCAGAC 1932
Db 2052 ATCCCTGTCAATTAATAATCCCACTTCTTGGATCAACCAAGTCAAGCTCAAGCCAGAC 2111
QY 1933 ACAATTTGTCAGCAATCAAGGACATTAACATTTGTTCTGAAAAGGAGCTAGCGAAGGA 1992
Db 2112 ACAATTTGTCAGCAATCAAGGACATTAACATTTGTTCTGAAAAGGAGCTAGCGAAGGA 2171
QY 1993 GCCTTTGAAAAGTGTTCCTAGCTGAATGTATTAACCTGCTGCTGAGCAAGCAAGATC 2052
Db 2172 GCCTTTGAAAAGTGTTCCTAGCTGAATGTATTAACCTGCTGCTGAGCAAGCAAGATC 2231
QY 2053 TTGGTGGCAGTGAAGACCTCGAAGAGATGCAAGTGAACATGCAAGCAAGACTTCCACCGT 2112
Db 2232 TTGGTGGCAGTGAAGACCTCGAAGAGATGCAAGTGAACATGCAAGCAAGACTTCCACCGT 2291
QY 2113 GAGGCGAGCTCCTGACCAACCTTCAGCATGAGACATGCTCAAGTTCTATGGCGTCTGC 2172

Db 2292 GAGGCCAGCTCCCTGACCAACCTCAGCATGAGCACAATCGTCATGAGGCTGCG 2351
 Qy 2173 GTGGAGGCGGACCCCTCATCATGCTTTGAGTACATGAAAGCATGGGGACCTCAACAG 2232
 Db 2352 GTGGAGGCGGACCCCTCATCATGCTTTGAGTACATGAAAGCATGGGGACCTCAACAG 2411
 Qy 2233 TTCTCTGAGGACACAGGCGCCCTGATGCGGTGCTGATGGCTGAGGCAACCCGCCACGAA 2292
 Db 2412 TTCTCTGAGGACACAGGCGCCCTGATGCGGTGCTGATGGCTGAGGCAACCCGCCACGAA 2471
 Qy 2293 CTGACGAGTGCAGATGCTGCAATATAGCCAGAGATCGCGCGGAGATGCTTACCTG 2352
 Db 2472 CTGACGAGTGCAGATGCTGCAATATAGCCAGAGATCGCGCGGAGATGCTTACCTG 2531
 Qy 2253 GCGGCCAGGACCTCGGACACCGGATTTGGGCAACAGGAACTGCTGTCGGGAGAAC 2412
 Db 2532 GCGGCCAGGACCTCGGACACCGGATTTGGGCAACAGGAACTGCTGTCGGGAGAAC 2591
 Qy 2413 TTGCTGTGAAAATCGGGGACTTTGGGATGTCCTGGGACGTGTACAGCACTGACTTAC 2472
 Db 2592 TTGCTGTGAAAATCGGGGACTTTGGGATGTCCTGGGACGTGTACAGCACTGACTTAC 2651
 Qy 2473 AGGGTCGTGGCCACACAAATGCTGCCCATTCGTGATGCTCCAGAGAGCATGATGAC 2532
 Db 2652 AGGGTCGTGGCCACACAAATGCTGCCCATTCGTGATGCTCCAGAGAGCATGATGAC 2711
 Qy 2533 AGGAAATTCACAGAGGAAAGGAGAGCTGAGAGCTGGGGGCTCGTGTGTGGAGATTTTC 2592
 Db 2712 AGGAAATTCACAGAGGAAAGGAGAGCTGAGAGCTGGGGGCTCGTGTGTGGAGATTTTC 2771
 Qy 2593 ACCTATGAGCAACAGCCCTGGTACAGCTGTCAAAACATGAGGATAGAGTATGATGACT 2652
 Db 2772 ACCTATGAGCAACAGCCCTGGTACAGCTGTCAAAACATGAGGATAGAGTATGATGACT 2831
 Qy 2653 CAGGGCCGAGTCTGACAGCCGACCCGACGTCGCCGAGAGAGTGTATGAGCTGATGCTG 2712
 Db 2832 CAGGGCCGAGTCTGACAGCCGACCCGACGTCGCCGAGAGAGTGTATGAGCTGATGCTG 2891
 Qy 2713 GGGTGTGAGGACGAGAGAGCCCAATAGAGAAACATCAAGGGCATTCATACCTGCTT 2772
 Db 2892 GGGTGTGAGGACGAGAGAGCCCAATAGAGAAACATCAAGGGCATTCATACCTGCTT 2951
 Qy 2773 CAGAACTTGGCCAAAGGATCTCCGGTCTACCTGACATTCAGAGCTTGGGCCCTTTTCCC 2832
 Db 2952 CAGAACTTGGCCAAAGGATCTCCGGTCTACCTGACATTCAGAGCTTGGGCCCTTTTCCC 3011
 Qy 2833 CAGACGATCTCTCCCAACGTAATCTCAGACGGGCTGAGAGATGAAACATCTTTAACT 2892
 Db 3012 CAGACGATCTCTCCCAACGTAATCTCAGACGGGCTGAGAGATGAAACATCTTTAACT 3071
 Qy 2893 GCCGCTGAGAGCCCAAGCTGCTCTCTCTTCACTGTGACAGTATTAACATCAAGACTCC 2952
 Db 3072 GCCGCTGAGAGCCCAAGCTGCTCTCTCTTCACTGTGACAGTATTAACATCAAGACTCC 3131
 Qy 2953 GAGAGGCTCTGAGGAAAGAGTGTACTTCTTCACTCACTCAAGTATTAACATCAAGACTCC 3012
 Db 3132 GAGAGGCTCTGAGGAAAGAGTGTACTTCTTCACTCACTCAAGTATTAACATCAAGACTCC 3191
 Qy 3013 TTTTGGATTAATCTCTTCTCTCTTCCATCTCCCTGGTGTGCTTTTCTTTTCTTTTAA 3072
 Db 3192 TTTTGGATTAATCTCTTCTCTCTTCCATCTCCCTGGTGTGCTTTTCTTTTCTTTTAA 3251
 Qy 3073 AATTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3132
 Db 3252 AATTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3311
 Qy 3133 GAATCATATGAGGCTTCTGCAATTAATCTGCAATGAGCAAGGCTTAAGAAAGCT 3192
 Db 3312 GAATCATATGAGGCTTCTGCAATTAATCTGCAATGAGCAAGGCTTAAGAAAGCT 3371
 Qy 3193 AATTTGTATATGAGAGACACTCCAGTTTCCACACCACTAAACATGCTTGTGTGA 3252

Db 3372 AATTTGTATATGAGAGACACTCCAGTTTCCACCAACCACTAAACATGCTTGTGTGA 3431
 Qy 3253 TTCCTGCTTTGATGTGATGATAAAGGAAACAAATATTTCACTTAACTTTGCA 3312
 Db 3432 TTCCTGCTTTGATGTGATGATAAAGGAAACAAATATTTCACTTAACTTTGCA 3491
 Qy 3313 CTTCTGCTTACAGATATGAGAGTTTCTATGATTTCACTTCTATTTATTTATTTATTT 3372
 Db 3492 CTTCTGCTTACAGATATGAGAGTTTCTATGATTTCACTTCTATTTATTTATTTATTT 3551
 Qy 3373 ACTGTTCTTATTTTGTGATGATGCTTAAACCTGTGTATTAAGAAACCTGTGTCA 3432
 Db 3552 ACTGTTCTTATTTTGTGATGATGCTTAAACCTGTGTATTAAGAAACCTGTGTCA 3611
 Qy 3433 ATCTGTAGACCTTTATCTATGAGATTAACCAAGAGAAAGAGATTTATATGA 3492
 Db 3612 ATCTGTAGACCTTTATCTATGAGATTAACCAAGAGAAAGAGATTTATATGA 3671
 Qy 3493 CCGCAATATGAGAGAAACAAAGCAACACTGGATCAGCTGTGTGACCTTACCTTAC 3552
 Db 3672 CCGCAATATGAGAGAAACAAAGCAACACTGGATCAGCTGTGTGACCTTACCTTAC 3731
 Qy 3553 GAATATCTCAGCACTGTTAGCTGGAGAAATGATTTGCGACCTTCCCTGAGACCTT 3612
 Db 3732 GAATATCTCAGCACTGTTAGCTGGAGAAATGATTTGCGACCTTCCCTGAGACCTT 3791
 Qy 3613 TCTGAGAGTAAAGAAAGCTAGCGCTCTGAGCAATGATTTCTTCCATCACAG 3672
 Db 3792 TCTGAGAGTAAAGAAAGCTAGCGCTCTGAGCAATGATTTCTTCCATCACAG 3851
 Qy 3673 AAATGATAGCGTCAGTAGAGAGCAAGATGCTT 3707
 Db 3852 AAATGATAGCGTCAGTAGAGAGCAAGATGCTT 3886

RESULT 10
 ADS92943
 ID ADS92943 standard; cDNA; 4057 BP.
 AC ADS92943;
 XX 02-DEC-2004 (first entry)
 XX
 DE Neurotrophic tyrosine kinase receptor type 2 cDNA.
 XX
 KW cytotraetic; gene therapy; human;
 KW branching morphogenesis modulating agent; MBM agent; gene; ss.
 OS Homo sapiens.
 XX
 PN W02004037990-A2.
 XX
 PD 06-MAY-2004.
 XX
 PF 22-OCT-2003; 2003MO-US033549.
 XX
 PR 23-OCT-2002; 2002US-0420554P.
 PR 30-DEC-2002; 2002US-0436941P.
 XX
 PA (EXEL-) EXELIXIS INC.
 XX
 PI Plozman GD, Karim PD, Swimmer C, Habeck HA, Koblizek TI,
 PI Schulte-Welker S, Langheinrich U, Stott GM, Trowe T, Vogel AM,
 PI Odenhal JH, Scheel JK, Will TT, Jin Y, Bjerke LM, Hal B,
 PI Adamkiewicz JI, Lickteig K, Hammonds RGR, Amundsen CD, Zhang H;
 PI Nicoll M;
 XX
 DR WPI: 2004-365506/34.
 DR P-PSDB; ADS92974.
 XX
 PT Identifying a candidate branching morphogenesis modulating agent for
 PT treating cancer comprises contacting the assay system comprising a MBM
 PT polypeptide or nucleic acid with a test agent and detecting a test agent-

PT biased activity.
XX
XX Example 3, SEQ ID NO 14, 179pp; English.
CC The invention describes a method of identifying a candidate branching
CC morphogenesis modulating (MBM) agent. The method comprises: providing an
CC assay system comprising a MBM polypeptide or nucleic acid; contacting the
CC assay system with a test agent under conditions where the system provides
CC a reference activity, except for the presence of the test agent; and
CC detecting a test agent-biased activity of the assay system, where a
CC difference between the test agent-biased activity and the reference
CC activity identifies the test agent as a candidate branching morphogenesis
CC modulating agent. Also described are: a method of modulating branching
CC morphogenesis in a mammalian cell; and a method for diagnosing a disease
CC in a patient. The method is useful in identifying a candidate branching
CC morphogenesis modulating agent for preparing a composition for diagnosing
CC or treating cancer. This sequence encodes a human branching morphogenesis
CC modulating (MBM) protein.
XX
SQ Sequence 4057 BP; 1013 A; 1033 C; 1014 G; 997 T; 0 U; 0 Other;
Query Match 98.4%; Score 3649; DB 13; Length 4057;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 3707; Conservative 0; Mismatches 0; Indels 48; Gaps 1;
QY 1 CCCCATTCCGATCTTAACAGAAATCTGCGCCCAAGAGTCCCGACGCCCGCTCGG 60
DB 132 CCCCATTCCGATCTTAACAGAAATCTGCGCCCAAGAGTCCCGACGCCCGCTCGG 191
QY 61 TGCCCGGCGCGCGCGCATGCAAGCAAGCGCGCGCGCGAGCTCCGAGCAGCGGTAGCGC 120
DB 192 TGCCCGGCGCGCGCGCATGCAAGCAAGCGCGCGCGAGCTCCGAGCAGCGGTAGCGC 251
QY 121 CCCCCTGTAAAGCGGTTCTGATGCGCGGACCACTGTGAACCTTGCCTGCGCGGAACA 180
DB 252 CCCCCTGTAAAGCGGTTCTGATGCGCGGACCACTGTGAACCTTGCCTGCGCGGAACA 311
QY 181 CTCTTCGCTCCGACCAAGCTCAGCTCTGATTAAGCTGAGCTCGGCAAGCCCGCAACAGC 240
DB 312 CTCTTCGCTCCGACCAAGCTCAGCTCTGATTAAGCTGAGCTCGGCAAGCCCGCAACAGC 371
QY 241 ACCGAGAGATTAAAGAGCGGCAAGCGGAGGAGGCTCCCGGCAAGCGGTGGGGAAG 300
DB 372 ACCGAGAGATTAAAGAGCGGCAAGCGGAGGAGGCTCCCGGCAAGCGGTGGGGAAG 431
QY 301 CGGCGGTGCAAGCGCGGGAAGGCACTCGGCTGAGCACTGCTGAGGATGCTGCTCC 360
DB 432 CGGCGGTGCAAGCGCGGGAAGGCACTCGGCTGAGCACTGCTGAGGATGCTGCTCC 491
QY 361 TGAATTAAGTGGCATGGAACCCGCAATGCGCGCTCTGGGCTTCTGCTGGCTGGTGTG 420
DB 492 TGAATTAAGTGGCATGGAACCCGCAATGCGCGCTCTGGGCTTCTGCTGGCTGGTGTG 551
QY 421 GGCCTTCGAGAGGCGCGCTTTCGCTGCGCAAGCTCGGCAATGCAAGTCTCTCGGATC 480
DB 552 GGCCTTCGAGAGGCGCGCTTTCGCTGCGCAAGCTCGGCAATGCAAGTCTCTCGGATC 611
QY 481 TGGTGCAGCGACCTTCTCTGCGATCGTGGCATTTCCGAAATTGAGCTTAACAGTGA 540
DB 612 TGGTGCAGCGACCTTCTCTGCGATCGTGGCATTTCCGAAATTGAGCTTAACAGTGA 671
QY 541 GATCTTGAGAACATCACCGAAATTTTCATGCAAAACGAAAGATTAGAAATCATCAAC 600
DB 672 GATCTTGAGAACATCACCGAAATTTTCATGCAAAACGAAAGATTAGAAATCATCAAC 731
QY 601 GAAATGATGTTGAAGCTTAATGAGGAGTGAAGAAATCTGACAAATTTGAGATTCTGA 660
DB 732 GAAATGATGTTGAAGCTTAATGAGGAGTGAAGAAATCTGACAAATTTGAGATTCTGA 791
QY 661 AATTTTGGCTCATTAAGCATTTCTGAAAAACAGCAACTGACGACATCAATTTTACC 720
DB 792 AATTTTGGCTCATTAAGCATTTCTGAAAAACAGCAACTGACGACATCAATTTTACC 851

QY 721 CGAAACAACTGACGAGTTTGTCTAGAAAATTTCCGACACTTGACTTGTGAACTG 780
DB 852 CGAAACAACTGACGAGTTTGTCTAGAAAATTTCCGACACTTGACTTGTGAACTG 911
QY 781 ATCTGGTGGGCAATCATTTTATCATGCTCTGTGACATTAATGAGTCAAGCTTCCAA 840
DB 912 ATCTGGTGGGCAATCATTTTATCATGCTCTGTGACATTAATGAGTCAAGCTTCCAA 971
QY 841 GAGGCTAAATCCAGTCCAGCACTCAGAGTTTGTACTGCTGAATGAAGACCAAGAT 900
DB 972 GAGGCTAAATCCAGTCCAGCACTCAGAGTTTGTACTGCTGAATGAAGACCAAGAT 1031
QY 901 ATTCCCTGGCAAACTCTGAGATACCCCAATTTGGTTTGGCATCTGCAATCTGGCCGCA 960
DB 1032 ATTCCCTGGCAAACTCTGAGATACCCCAATTTGGTTTGGCATCTGCAATCTGGCCGCA 1091
QY 961 CTTAACCTCATGTGAGAGAAAGTCTATCATATTATCTGTAGTGGCAGGTGAT 1020
DB 1092 CTTAACCTCATGTGAGAGAAAGTCTATCATATTATCTGTAGTGGCAGGTGAT 1151
QY 1021 CCGGTTCTTAATATGATTTGGAGTGTGTACCTGGTTTCCAAACATATGAATGAACA 1080
DB 1152 CCGGTTCTTAATATGATTTGGAGTGTGTGTACCTGGTTTCCAAACATATGAATGAACA 1211
QY 1081 AGCCACACAGGCGCTCTTAAGGATTAATCAATTTTATCCGATGACAGTGGGAAGCAG 1140
DB 1212 AGCCACACAGGCGCTCTTAAGGATTAATCAATTTTATCCGATGACAGTGGGAAGCAG 1271
QY 1141 ATCTCTTGTGTGCGGAAATCTTGTAGGAGAAATCAAGATCTGTGCAACTCATGTG 1200
DB 1272 ATCTCTTGTGTGCGGAAATCTTGTAGGAGAAATCAAGATCTGTGCAACTCATGTG 1331
QY 1201 CATTTTGACCAATATATCAATTTCTGAATCTCCAACTCAGACCACTGAGTCAAT 1260
DB 1332 CATTTTGACCAATATATCAATTTCTGAATCTCCAACTCAGACCACTGAGTCAAT 1391
QY 1261 CCAATCACTGTGAAGGCAACCCCAACCGCGCTTCAAGTGTCTTAATCGGGCAATA 1320
DB 1392 CCAATCACTGTGAAGGCAACCCCAACCGCGCTTCAAGTGTCTTAATCGGGCAATA 1451
QY 1321 TTGAATGAGTCCAAATATCATCTGAATCAATATCATGTTACCAATCAACGAGATAC 1380
DB 1452 TTGAATGAGTCCAAATATCATCTGAATCAATATCATGTTACCAATCAACGAGATAC 1511
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Db 3852 AAATGATAGCGTGAAGAGAGCAAGATGAGCTT 3886

RESULT 11
AAT00689
ID AAT00689 standard; DNA; 3194 BP.
XX
AC AAT00689;
XX
DT 31-MAR-1996 (first entry)
XX
XX Human trkB receptor DNA.
DE
XX trkB receptor; tyrosine-kinase; enzyme; protease; inflammation; pain;
KM diagnosis; neurotrophic factor; kidney; lung; psychiatric disorder; 88.
XX
OS Homo sapiens.

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PN	WO9525795-A1.	
XX	28-SEP-1995.	
PD		
XX	17-MAR-1995;	95WO-US003426.
XX		
XX	18-MAR-1994;	94US-00215139.
PR	05-AUG-1994;	94US-00286846.
PR	20-DEC-1994;	94US-00359705.
XX		
PA	(GETH) GENENTECH INC.	
XX		
PJ	Presta LG, Shelton DL, Uffler R;	
XX		
XX	WPI, 1995-344616/44.	
DR	P-PsDB; AAR81630.	
XX		
PT	New human trkA and trkC poly(peptide(s) and fusion proteins contg. them - -	
PT	also DNA, vectors and transformed cells useful in treatment and diagnosis	
PT	of abnormal neurotrophic factor expression, e.g. inflammatory pain.	
XX		
PS	Claim 8; Fig 1A-B; 117pp; English.	
XX		
CC	This DNA sequence may be expressed recombinantly for the production of	
CC	human trkC receptor, and to detect or amplify trkC genes. The encoded	
CC	protein may be used as a reagent in kinase receptor activation assays,	

CC	and therapeutically in diseases associated with over or under expression
CC	of neurotrophic factor (e.g. pain of inflammation, kidney, lung,
CC	cardiovascular or psychiatric disorders and some sorts of tumours)
XX	
XX	
Sequence	3194 BP; 824 A; 793 C; 761 G; 816 T; 0 U; 0 Other;
Query Match	85.2%; Score 3156.6; DB 2; Length 3194;
Best Local Similarity	99.7%; Fred. No. 0;
Matches 3162;	Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY	252 AAGAGAGCCGGAAGGACGAGGAAAGGCGCTCCCGGACGGGTGGGGAAGCGCGCGTGC
DB	14 AAGAAAGCGGCAAGCGGACGAGGAAAGGCGCTCCCGGACGGGTGGGGAAGCGCGCGTGC
QY	312 GCGCGGGGACAGGACCTCGGCGCTGGCACTGCGCTGTAGGAATGTCTCTGGATTAAGTG
DB	74 GCGCGGGGACAGGACCTCGGCGCTGGCACTGCGCTGTAGGAATGTCTCTGGATTAAGTG
QY	312 GCATGGACCCGCGCATGGCGCGGCTTCTGGGGCTTCTGCTGTGTGTGGGCTTCTGGAG
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DB	254 CCCTTCTCTCGGACCTGTGGCATTTCCGAGATTGGAGCTTAACAGTGTAGTCTTGAGAA
QY	552 CATCACCGAAATTTTCATCCGCAACAGAAAGGTTAGAAATTCATCAACGAAGATGATGT
DB	314 CATCACCGAAATTTTCATCCGCAACAGAAAGGTTAGAAATTCATCAACGAAGATGATGT
QY	612 TGAAGCTTATGTGGGACTGAGAAATCTGACATTTGTGATTTCTGGATTAAATTTGTGGC
DB	374 TGAAGCTTATGTGGGACTGAGAAATCTGACATTTGTGATTTCTGGATTAAATTTGTGGC
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DB	434 TCATTAAGCATTTCTGAATAAACAGCAACCTGCAGACATCAATTTTACCCGAAACAACT
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DB	494 GACGAGTTTGTCTAGGAAACATTTCCGTCACCTTGACTTGTCTGAACTGATCTGTGTGGG
QY	792 CAATCATTTTCAATGCTCTGTGACATTAATGTGATCAAGACTCTCCAAAGAGGCTTAATCT
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QY	852 CAGTCAGACACTCGAGATTTGTATCTGCTGCTGAATGAAGACAGCAAGATATTTCCCTGAC
DB	614 CAGTCAGACACTCGAGATTTGTATCTGCTGCTGAATGAAGACAGCAAGATATTTCCCTGAC
QY	912 AAACCTGAGATACCCAAATTTGGTTTGGCATCTGCAATCTGGCGGACCTTAACCTCAC
DB	674 AAACCTGAGATACCCAAATTTGGTTTGGCATCTGCAATCTGGCGGACCTTAACCTCAC
QY	972 TGTGAGAGAAAGGAAGTCTATCACTTAATCCGTAGTGTGGCAGGTAATCCGGTTCCTAA
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DB	794 TATGATTTGGGATGTGTGTTAACTGGTTTCCAAACATATGATGAATGAACGACACACA
QY	1092 GGGCTCTTTAAGGATTAACATTTTCAATCCGATGACAGTGGGAAGCAGATCTCTTGTGT
DB	854 GGGCTCTTTAAGGATTAACATTTTCAATCCGATGACAGTGGGAAGCAGATCTCTTGTGT
QY	1152 GCGGGAATCTTGTAGAGAAAGATCAAGATTTCTGTCAACCTCACTGTGCATTTTGGACC
DB	914 GCGGGAATCTTGTAGAGAAAGATCAAGATTTCTGTCAACCTCACTGTGCATTTTGGACC

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Qy 3372 TACTGTCTTATTTGTTTGGATGCTTAAGCTGTGTATTAAGAAAAAGAAA 3422

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RESULT 12
AAZ88839
ID      AAZ88839 standard; DNA; 3194 BP.
XX
AC      AAZ88839;
XX
DT      30-MAY-2000 (first entry)
XX
DE      Human trkB receptor DNA.
XX
KM      trkB; human; receptor tyrosine kinase; trkC; diagnosis; neurotrophin;
KW      neurotrophic factor; db.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
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FT              /product= "trkB receptor"
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PN      US6027927-A.
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PD      22-FEB-2000.
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PF      01-OCT-1997; 97US-00942562.
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PR      18-MAR-1994; 94US-00215139.
PR      05-AUG-1994; 94US-00286846.
PR      19-MAY-1995; 95US-00444597.
XX
PA      (GETH ) GENENTECH INC.
XX
PI      Uffer R, Shelton DL, Presta LG;
DR      WPI; 2000-194832/17.
DR      P-PSDB; AAY51599.
XX
PT      New human trk receptors useful in the diagnosis of various human
PT      pathological conditions associated with elevated or reduced levels of
PT      neurotrophins capable of binding trkB and/or trkC.
XX
PS      Disclosure; Col 59-64; 78pp; English.
XX
CC      This invention describes a novel isolated and purified polypeptide (1),
CC      belonging to the trk family of receptor tyrosine kinases, trkB and trkC.
CC      (1) are useful in the purification of human neurotrophic factors and in
CC      the diagnosis of various human pathological conditions associated with
CC      elevated or reduced levels of neurotrophins capable of binding trkB
CC      and/or trkC. This sequence encodes the human trkB receptor described in
CC      the method of the invention
XX
SQ      Sequence 3194 BP; 824 A; 793 C; 761 G; 816 T; 0 U; 0 Other;
Query Match      85.2%; Score 3156.6; DB 3; Length 3194;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3162; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY      252 AAGAGAGCCGCAAGCGAGGAGGCTCCCGCAGCGGCTGGGAGAAAGCGCCGTCGA 311
Db      14 AAGAGAGCCGCAAGCGAGGAGGAGGCTCCCGCAGCGGCTGGGAGAAAGCGCCGTCGA 73
QY      312 GCGGCGGAGACAGGACTCGGGCTGGCACTGGCTGTAGGAGATGTCGCTCGAATAAGTG 371
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QY      432 GCGCGCTTTCGCTGTCACGTCCTGCAATGACAGTGCCTCGGATCTGTGACGCGA 491
Db      194 GCGCGCTTTCGCTGTCACGTCCTGCAATGACAGTGCCTCGGATCTGTGACGCGA 253
QY      492 CCTTCTCCGATGATGAGCATTTTCGAGATTGAGACCTTAAGAGTATCTTGAGAA 551
Db      254 CCTTCTCCGATGATGAGCATTTTCGAGATTGAGACCTTAAGAGTATCTTGAGAA 313
QY      552 CATACCGAAATTTTCATGCGCAACGAAAGGTTGAAATCATCAACGAGATGATGT 611
Db      314 CATACCGAAATTTTCATGCGCAACGAAAGGTTGAAATCATCAACGAGATGATGT 373
QY      612 TGAAGCTTATGAGGAGCTGAGAAATCGAACATTTGAGATTCTGATTAATTTGGGC 671
Db      374 TGAAGCTTATGAGGAGCTGAGAAATCGAACATTTGAGATTCTGATTAATTTGGGC 433
QY      672 TCATTAAGCATTTCTGAAAAACAGCAACCTGCAGACATCAATTTTAACCGAACAACT 731
Db      434 TCATTAAGCATTTCTGAAAAACAGCAACCTGCAGACATCAATTTTAACCGAACAACT 493
QY      732 GACGAGTTGTCTAGAGAAACATTTCCGTGACCTTGAATTGTCTGAACCTGCTGGGG 791
Db      494 GACGAGTTGTCTAGAGAAACATTTCCGTGACCTTGAATTGTCTGAACCTGCTGGGG 553
QY      792 CAATCCATTTACATGCTCCCTGTCACATTAATGAGATCAAGACTCTCAGAGGCTAAATC 851
Db      554 CAATCCATTTACATGCTCCCTGTCACATTAATGAGATCAAGACTCTCAGAGGCTAAATC 613
QY      852 CAGTCCAGACACTCAGGATTTGTACTGCTGATGAGAAAGCAGAGAAATTTCCCTGGC 911
Db      614 CAGTCCAGACACTCAGGATTTGTACTGCTGATGAGAAAGCAGAGAAATTTCCCTGGC 673
QY      912 AAACCTGAGATACCAATTTGTTGCTTCATCTGCAATCTGGCGACCTTAACCTGAC 971
Db      674 AAACCTGAGATACCAATTTGTTGCTTCATCTGCAATCTGGCGACCTTAACCTGAC 733
QY      972 TGTGAGAGAGAAAGATCTATCAATTATCTGTAGTGGGAGAGATTCGGTTCTTA 1031
Db      734 TGTGAGAGAGAAAGATCTATCAATTATCTGTAGTGGGAGAGATTCGGTTCTTA 793
QY      1032 TATGTATGGAGATGTTGTAACTCGGTTTCAAACTATATGAAACAGACACACA 1091
Db      794 TATGTATGGAGATGTTGTAACTCGGTTTCAAACTATATGAAACAGACACACA 853
QY      1092 GGGCTCCTTAAGATTAATCAATTTATCCGATGACAGTGGAGAGATCTCTGTGT 1151
Db      854 GGGCTCCTTAAGATTAATCAATTTATCCGATGACAGTGGAGAGATCTCTGTGT 913
QY      1152 GCGGAAATCTGTGAGAGAAATCAAGATCTGTCAACTCACTGTGCAATTTTGACC 1211
Db      914 GCGGAAATCTGTGAGAGAAATCAAGATCTGTCAACTCACTGTGCAATTTTGACC 973
QY      1212 AACTATCACTTCTGGAATCTCAACTCAGACCACTGAGTGCATTCATTCAGTGT 1271
Db      974 AACTATCACTTCTGGAATCTCAACTCAGACCACTGAGTGCATTCATTCAGTGT 1033
QY      1272 GAAAGCAACCCCAACCAAGCGCTTCAAGTGTCTATTAACGGGCAATATGATGATC 1331
Db      1034 GAAAGCAACCCCAACCAAGCGCTTCAAGTGTCTATTAACGGGCAATATGATGATC 1093
QY      1332 CAATATCATTTGTACTTAATAATATATGATTCATCAACGAGATCAACGAGCTCTCCA 1391
Db      1094 CAATATCATTTGTACTTAATAATATATGATTCATCAACGAGATCAACGAGCTCTCCA 1153
QY      1392 GCTGATTAATCCCACTCACTGAACAATGGGAGCTCACTTAATAGCCAAAGATGATGA 1451
Db      1154 GCTGATTAATCCCACTCACTGAACAATGGGAGCTCACTTAATAGCCAAAGATGATGA 1213
QY      1452 TGGGAAAGATGAGAAACAGATTTCTGCTCACTTCATGAGGCTGGCTGGAATGACATGG 1511
Db      1214 TGGGAAAGATGAGAAACAGATTTCTGCTCACTTCATGAGGCTGGCTGGAATGACATGG 1273
QY      1512 TGCAAACCCCAATTAATTCGATGATTAATTAAGAAATATGAACTGCAGCGAAATGACAT 1571
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Db	1274	TCGAACCCTTAATATCTGTGATGTAATTAATGAAGATTATGAACCTGACGGAAATGACAT	1333
Oy	1572	CGGGGACACACGACGAAAGAGTAATGAAATCCCTTCCACAGACCTCACTGATTAACCGG	1631
Db	1334	CGGGGACACACGACGAAAGAGTAATGAATCCCTTCCACAGACCTCACTGATTAACCGG	1393
Oy	1632	TCGGGAACATCTTCGTGGCTATAGCTGTGGTGGTGAATGCGTCTGTGGTGGGATTTTGCT	1691
Db	1394	TCGGGAACATCTTCGTGGCTATAGCTGTGGTGGTGAATGCGTCTGTGGTGGGATTTTGCT	1453
Oy	1692	TTTGGTATAGCTGTTTCGTTAAGTTGGCAAGACCTCCAAAGTTGGCATGAAGGCC	1751
Db	1454	TTTGGTATAGCTGTTTCGTTAAGTTGGCAAGACCTCCAAAGTTGGCATGAAGGCC	1513
Oy	1752	AGCCTCCGTTATACGAATGATGATGACTGTGCAGGCCCTCCATCATCTCCAAATG	1811
Db	1514	AGCCTCCGTTATACGAATGATGATGACTGTGCAGGCCCTCCATCATCTCCAAATG	1573
Oy	1812	GAGTAACACTCATCTTCTTCGGAAGGTGGCCAGATGCTGTCAATTAATGGAATGACCA	1871
Db	1574	GAGTAACACTCATCTTCTTCGGAAGGTGGCCAGATGCTGTCAATTAATGGAATGACCA	1633
Oy	1872	GATCCCTGTCAATTGAAAATTCGCCAGTACTTTGGCATACCAACAGTCAGCTCAAGCCAGA	1931
Db	1634	GATCCCTGTCAATTGAAAATTCGCCAGTACTTTGGCATACCAACAGTCAGCTCAAGCCAGA	1693
Oy	1932	CACATTTGTCAGGCATCAAGCCGACATPAACATTTGTTGAAAAGGGAGCTAGGCGAAG	1991
Db	1694	CACATTTGTCAGGCATCAAGCCGACATPAACATTTGTTGAAAAGGGAGCTAGGCGAAG	1753
Oy	1992	AGCCTTTGAAAAGGTGTTCTAGCTGAATGCTATACTGTGCTGTGACAGACAAGAT	2051
Db	1754	AGCCTTTGAAAAGGTGTTCTAGCTGAATGCTATACTGTGCTGTGACAGACAAGAT	1813
Oy	2052	CTTGTGTGCATGAAGACCTTGAAGAGATGCCAGTGAACAATGACGCAAGGACTTCCACG	2111
Db	1814	CTTGTGTGCATGAAGAGCTTGAAGAGATGCCAGTGAACAATGACGCAAGGACTTCCACG	1873
Oy	2112	TGAGGCGAGGCTCCCGAACACCTGCACATGAGACATGCGTCAAGTTCTATGGCGTCTG	2171
Db	1874	TGAGGCGAGGCTCCCGAACACCTGCACATGAGACATGCGTCAAGTTCTATGGCGTCTG	1933
Oy	2172	CGTGAAGGGCGACCCCTCATCATGATGTTTGAAGTACATGAAGCATGGGGACCTCAACA	2231
Db	1934	CGTGAAGGGCGACCCCTCATCATGATGTTTGAAGTACATGAAGCATGGGGACCTCAACA	1993
Oy	2232	GTTCTCAAGGGCACAGGCGCTTGATGCGGTGTGATGAGCTGAGGGCAACCGGCCACGA	2291
Db	1994	GTTCTCAAGGGCACAGGCGCTTGATGCGGTGTGATGAGCTGAGGGCAACCGGCCACGA	2053
Oy	2292	ACTGACGAGTGCAGATGCTGCAATATAGCCAGAGATTCGCGGGGCATATGTTACTT	2351
Db	2054	ACTGACGAGTGCAGATGCTGCAATATAGCCAGAGATTCGCGGGGCATATGTTACTT	2113
Oy	2352	GCGCGTCCAGCACTTGTGCAACCGGATTTTGGCCACACGAACTGCTGTGCGGGAGAA	2411
Db	2114	GCGCGTCCAGCACTTGTGCAACCGGATTTTGGCCACACGAACTGCTGTGCGGGAGAA	2173
Oy	2412	CTTGTGTGTGAATAATCGGGGACTTTGGGATGTCCCGGAGCGTGACAGCACTGACTACTA	2471
Db	2174	CTTGTGTGTGAATAATCGGGGACTTTGGGATGTCCCGGAGCGTGACAGCACTGACTACTA	2233
Oy	2472	CAGGGTCCGTGGCCACAACAATGCTGCCAATTCGCTGATATGCTCCAGAGAGATCATATGA	2531
Db	2234	CAGGGTCCGTGGCCACAACAATGCTGCCAATTCGCTGATATGCTCCAGAGAGATCATATGA	2293
Oy	2532	CAGGAAATTCACGACGGAAGGAGAGGTCTGAGACTGTGGGGGTCTGTGTGTGGAGATTTT	2591
Db	2294	CAGGAAATTCACGACGGAAGGAGAGGTCTGAGACTGTGGGGGTCTGTGTGTGGAGATTTT	2353
Oy	2592	CACCTATGGCAACAGCCTGTGTACAGCTGTCAACAATGAGTGTATAGTGTATCAC	2651

Db	2254	CACCTATATGGCAAAACAGCCCTGTGTACACGCTGTCAAAACAATGAGGTGATGATGCTGATCAC	2413
Qy	2552	TCAGGCGCCGAGATCCTGTGACGACGACCCCGACGTCGCCCGAGAGGTGTATGAGCTGATGCT	2711
Db	2414	TCAGGCGCCGAGATCCTGTGACGACGACCCCGACGTCGCCCGAGAGGTGTATGAGCTGATGCT	2473
Qy	2712	GGGGTGTCTGGAGGAGGAGGCCCACTATGAGGAAGAAACATCAAGGGCAATCCATACCCTCT	2771
Db	2474	GGGGTGTCTGGAGGAGGAGGCCCACTATGAGGAAGAAACATCAAGGGCAATCCATACCCTCT	2533
Qy	2772	TCAGAACTTGGCCCAAGGAGCATCTCCGGTCTACCTGGACATTTCTAGGCTTAGGGCCCTTTTTC	2831
Db	2554	TCAGAACTTGGCCCAAGGAGCATCTCCGGTCTACCTGGACATTTCTAGGCTTAGGGCCCTTTTTC	2593
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Db	2594	CCAGACCGATCCCTTCCCAACGTAATCCTCTCAGACGCGGCTGAGAGATGAAATCTTTTAAC	2653
Qy	2882	TGCGGCTTGGAGGCCCAACGCTGCTCTCTCTCACTGTGACAGTATTAACATCAAGATC	2953
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Qy	2952	CGAGAAAGCTTCGAGGGGAAGAGTGTACTTCTTCAATCAATPAGACAGATTTGACTTC	3011
Db	2714	CGAGAAAGCTTCGAGGGGAAGAGTGTACTTCTTCAATCAATPAGACAGATTTGACTTC	2773
Qy	3012	TTTTTGGCATTAATCTCTTCTCTCTTTCATCTCCCTTGATGTTCCTTTTCTTTT	3071
Db	2774	TTTTTGGCATTAATCTCTTCTCTCTTTCATCTCCCTTGATGTTCCTTTTCTTTT	2833
Qy	3072	AAATTTTCTTTTCTTCTTCTTTTTCCTTTCCTTCCGCTTCAAGATTTTACCCTTCTT	3133
Db	2834	AAATTTTCTTTTCTTCTTCTTTTTCCTTTCCTTCCGCTTCAAGATTTTACCCTTCTT	2893
Qy	3132	TGAATCAATCTGGGCTTGTGATTAATTAATCTGTGATPAGCAAAAGGCTTAAACAAG	3193
Db	2894	TGAATCAATCTGGGCTTGTGATTAATTAATCTGTGATPAGCAAAAGGCTTAAACAAG	2953
Qy	3192	TAAATTTGTAATATACAGACAGACATCTCAGATTTGCCCAACAACATAAGTCCCTTGTGT	3253
Db	2954	TAAATTTGTAATATACAGACAGACATCTCAGATTTGCCCAACAACATAAGTCCCTTGTGT	3013
Qy	3252	ATTCTCGCTTGTGATGTGATGAAAAAAGGAAAAACAATTTTCACTTAACTTTGTC	3313
Db	3014	ATTCTCGCTTGTGATGTGATGAAAAAAGGAAAAACAATTTTCACTTAACTTTGTC	3073
Qy	3312	ACTTGTGCTGACAGATATACAGAGTTTCTATGATTAATCACTTATTAATTAATAT	3373
Db	3074	ACTTGTGCTGACAGATATACAGAGTTTCTATGATTAATCACTTATTAATTAATAT	3133
Qy	3372	TACTGTTCCTATTTGTTTTTGGATGGCTTAAGCCTGTGTATTAAGAAAAA 3422	
Db	3134	TACTGTTCCTATTTGTTTTTGGATGGCTTAAGCCTGTGTATTAAGAAAAA 3184	
RESULT 13			
AAT51457			
ID AAT51457 standard; DNA; 3060 BP.			
AAT51457;			
AC			
XX			
XX			
DT	16-OCT-2003	(revised)	
DT	27-AUG-2003	(revised)	
DT	30-APR-1997	(first entry)	
XX			
XX			
DE	gD.tcrb fusion useful in kinase receptor activation assay.		
XX			
KW	kinase receptor activation; KIRA; receptor protein tyrosine kinase; rPTK;		
KW	signal transduction; autophosphorylation; gD.tcrb;		
KW	enzyme-linked immunosorbent assay; ELISA; de.		
XX			
OS	Human herpesvirus 1.		
OS	Homo sapiens.		

```
OS Chimeric.
XX
FH Key Location/Qualifiers
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FT /note= "sp6 RNA start"
FT misc_RNA 79
FT /*tag= b
FT /note= "begin gd from pchadIII"
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FT /*tag= f
FT /note= "SV40 early polyA"
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XX
PD 01-JUN-1995.
XX
PF 18-NOV-1994; 94WO-US013329.
XX
PR 23-NOV-1993; 93US-00157563.
PR 20-DEC-1993; 93US-00170558.
PR 05-AUG-1994; 94US-00286305.
XX
PA (GETH ) GENENTECH INC.
XX
PI Godowski PJ, Mark MR, Sadiq MD, Wong WLT;
XX
DR WPI: 1995-207042/27.
XX
DR P-PSDB; AAM11941.
XX
PT Measuring auto-phosphorylation of tyrosine kinase receptor - to identify
XX and characterise potential (ant)agonists of TKR.
XX
PS Example 3; Fig 13a-g; 148bp; English.
XX
XX DNA constructs (AAT51456-58) respectively code for gd.trkA (AAM11940),
XX gd.trkB (AAM11941) and gd.trkC (AAM11942), comprising fusions between
XX herpes simplex virus glycoprotein D flag polypeptide and human receptor
XX protein tyrosine kinases (trPKs) trkA, B and C, which are involved in the
XX interaction between neurotrophins and their target cells. The gd.trk
XX constructs can be expressed e.g. in dp12.CHO host cells and used in
XX kinase receptor activation, enzyme-linked immunosorbent assays (ELISA
XX ELISA) to measure autophosphorylation of trPK kinase domains. These
XX assays are used to identify and characterise potential (ant)agonists of
XX trPKs, study ligand-receptor interactions, measure phosphatase activity
XX and identify trPK ligands in clinical samples. (Updated on 27-AUG-2003 to
XX correct OS field.) (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 3060 BP; 782 A; 804 C; 744 G; 730 T; 0 U; 0 Other;
Query March 67.9%; Score 2516.2; DB 2; Length 3060;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2518; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 445 TGTCCACGCTCTGCAATGAGTGCCTCTGGAATCTGTGACAGACCTTCTCTGGC 504
Db 475 TGTCCACGCTCTGCAATGAGTGCCTCTGGAATCTGTGACAGACCTTCTCTGGC 534
QY 505 ATCGTGCAATTCGAGATTGAGAGCTTAACAGTGTAGATCTTGAGAAATCAGCGAAATT 564
Db 535 ATCGTGCAATTCGAGATTGAGAGCTTAACAGTGTAGATCTTGAGAAATCAGCGAAATT 594
QY 565 TTGATCGCAACCGAAGAGTTAGAAATCATCAACGAAGATGATGTTGAAGCTTAATGTG 624
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Db 595 TTGATCGCAACCGAAGAGTTAGAAATCATCAACGAAGATGATGTTGAAGCTTAATGTG 654
QY 625 GAGCTGAGAAATCTGACAAATTTGTGAAATTTGAAATTTTGTGCTCATTAAGCATTT 684
Db 655 GAGCTGAGAAATCTGACAAATTTGTGAAATTTGAAATTTTGTGCTCATTAAGCATTT 714
QY 685 CTGAAAAACGCAACCTGAGCAATCAATTTTACCAGAAACAAATCAGAGATTGTCT 744
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Db 895 CAGATTTGTACTGCTGCTGAAATGAAAGAGCAAAATTTTCCCTGGCAACCTGCAGATA 954
QY 925 CCCAATTTGTTGGTTCATCTGCAAAATCTGACCGACCTTAACCTCACTGTGAGAGAGA 984
Db 955 CCCAATTTGTTGGTTCATCTGCAAAATCTGACCGACCTTAACCTCACTGTGAGAGAGA 1014
QY 985 AAGTCTATCACTTATCTGTAGTGTGAGAGTGTGATCCGGTTCCTAATATGATTTGGAT 1044
Db 1015 AAGTCTATCACTTATCTGTAGTGTGAGAGTGTGATCCGGTTCCTAATATGATTTGGAT 1074
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Db 1375 ACTAAATACATGTATTAACAATCAACAGAGTACCAACGGCTGCTCCAGCTGATTAATCCC 1434
QY 1405 ACTCACTGAACAAATGGGAGCTACCTTAATAGCCAAAGATGATTTGGAAAGATGAG 1464
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QY 1465 AAACAGATTTCTGTCACTTCAAGGGGCTGAGCTGGAATTTGACGATGTAACCCCAAT 1524
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Db 1555 TATCTGATGTAAATTTATGAAGATTATGAAATCTGACAGCAATGACATCGGGGACACCA 1614
QY 1585 AACAGAGTATGAATCCCTTCCACAGAGCTCACTGATTAACCCGGTGGGAAACATCTC 1644
Db 1615 AACAGAGTATGAATCCCTTCCACAGAGCTCACTGATTAACCCGGTGGGAAACATCTC 1674
QY 1645 TCGGTCTATGCTGTGTGTGATTTGAGCTCTGTGTGTGGAATTTTGGTGAATGCTG 1704
Db 1675 TCGGTCTATGCTGTGTGTGATTTGAGCTCTGTGTGTGGAATTTTGGTGAATGCTG 1734
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QY 1705 TTTCGCTTAAGTGGCAAGACCTCGAAGTTTGGCATGAAAGGCCAGCCTCCGTTATC 1764
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 DB 1795 AGCAATATATGATCTCTGCCAGCCACTCCATCAATCTTCCAAATGGAGTAACTTCCA 1854
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 DB 1855 TCTTCTTGGAAAGGTGGCCGAGATGCTGCTATTAATGGAAATGACCAAGATCCCGTCAAT 1914
 QY 1885 GAAATATCCCAAGTACTTTGGCATCAACAGTCAAGCTCAAGCAGACACTTTGTTGAG 1944
 DB 1915 GAAATATCCCAAGTACTTTGGCATCAACAGTCAAGCTCAAGCAGACACTTTGTTGAG 1974
 QY 1945 CACATCAAGGACATTAACATTTGTTCTGAAAAGGAGCTAGGCGAAGAGCTTTGGAAAA 2004
 DB 1975 CACATCAAGGACATTAACATTTGTTCTGAAAAGGAGCTAGGCGAAGAGCTTTGGAAAA 2034
 QY 2005 GTGTTCTAGCTGAATGTAATTAACCTGCTGCTAGAGAGGCAAGATCTTGTGTGAGCAGTG 2064
 DB 2035 GTGTTCTAGCTGAATGTAATTAACCTGCTGCTAGAGAGGCAAGATCTTGTGTGAGCAGTG 2094
 QY 2065 AAGACCTGAAGAGATGCGCAGTGAATGCAAGAGACTTCCACCGTGAAGGCCAGAGCTC 2124
 DB 2095 AAGACCTGAAGAGATGCGCAGTGAATGCAAGAGACTTCCACCGTGAAGGCCAGAGCTC 2154
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 QY 2305 CAGATGCTGATATATAGCCAGCAGATCGCGCGGCGATGCTCTGCTGCTGCCAGAC 2364
 DB 2335 CAGATGCTGATATATAGCCAGCAGATCGCGCGGCGATGCTCTGCTGCTGCCAGAC 2394
 QY 2365 TTGCTGACCGCCATTTTGGCCACAGAACTGCTGCTGCGGGAGAACTTCTGCTGAAA 2424
 DB 2395 TTGCTGACCGCCATTTTGGCCACAGAACTGCTGCTGCGGGAGAACTTCTGCTGAAA 2454
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 DB 2575 ACGGAAAGCGAGCTTGGAGCTTGGGGGTGCTGTTTGGGAGATTTTCACTTATGGCAA 2634
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 DB 2635 CAGCCCTGATACGAGCTGTCAAACATGAGGTGATAGGTATACACTCAGGGGCGAGTC 2694
 QY 2665 CTGAGAGGACCCCGCAGTGGCCCGCAGAGAGGTGTATGAGTGTGAGTGTGCTGAG 2724
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 QY 2725 CGAGAGCCCACTGAGAGAGAAATCAAGGGCATTCATACCTTCTTCAAGACTTGGCC 2784
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QY 2785 AAGGCACTCCCGGTCTACTGGAATTTCTAGAGCTTAGGGCCCTTTTCCCGACAGCATCT 2844
 DB 2815 AAGGCACTCCCGGTCTACTGGAATTTCTAGAGCTTAGGGCCCTTTTCCCGACAGCATCT 2874
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 QY 2965 A 2965
 DB 2995 A 2995
 RESULT 14
 ADB79772
 ID ADB79772 standard; DNA; 4757 BP.
 XX
 AC ADB79772;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Rat neural receptor protein-tyrosine kinase, trkB, DNA, SEQ ID 12.
 XX
 KW Analgesic; pain; streptozocin-induced diabetes; rat; gene; ds.
 XX
 OS Rattus norvegicus.
 XX
 EN EP1279744-A2.
 XX
 PD 29-JAN-2003.
 XX
 PE 26-JUL-2002; 2002EP-00255249.
 XX
 PR 27-JUL-2001; 2001GB-00018354.
 PR 07-FEB-2002; 2002GB-00002910.
 XX
 PA (WARN) WARNER LAMBERT CO.
 PI Brookbank RA, Dixon AK, Lee K, Pimock RD;
 XX
 DR WPI: 2003-395407/38.
 XX
 DR P-PSDB; ADB79771.
 XX
 PT Use of isolated gene sequences and encoded polypeptides that are
 PT upregulated in the spinal cord in response to streptozocin-induced
 PT diabetes for screening compounds for the treatment of pain, or for
 PT diagnosing pain.
 XX
 PS Claim 1; Page 57-58; 334pp; English.
 XX
 CC The present invention relates to nucleotide sequences which are useful in
 CC the screening of compounds for the treatment of pain, or for the
 CC diagnosis of pain. The nucleotide sequences are up-regulated in the
 CC spinal cord in response to streptozocin-induced diabetes. The present
 CC sequence is one such nucleotide sequence.
 XX
 SO Sequence 4757 BP; 1122 A; 1288 C; 1197 G; 1150 T; 0 U; 0 Other;
 Query Match 61.1%; Score 2264.2; DB 10; Length 4757;
 Best Local Similarity 79.5%; Pred. No. 0;
 Matches 2919; Conservative 0; Mismatches 618; Indels 134; Gaps 15;
 QY 74 GGGGCTATGCGGAGCGGCGCGCGGAGCTCCGAGCAGCGGTAGCGCCCTGTAAGC 133
 DB 390 GAGCCACCGAGTGGCGCTGCGGTATGAGACATGACGCGCCTTGTGGCTTGAAGAGC 449
 QY 134 GTTGTGCTATGCGGAGCACTGTAACCTGCGCGCTGCGGAACTCTTGGCTC--- 190
 DB 450 GGGCGGTATGTTCCAGCAGCTGTAACATTTGTGTAGGCGCAACTGTGCTCAGGCCGAG 509

OY	191	--CGAGCAGCTCAGCCTCTGTATTAAGCTGAGACTGGCAGCCGCCGACACAGACATCGAGGA	248
Db	510	CACCGACAGGGCTCAGCCCTCTGTGTACGCTCTCTCGGGGGAGGCGCATCAGACCC-----	563
OY	249	GTTTAAGAGAGCCGCGAAGCGCAGGGAAGGCGTCCCGCGACCGAGGTGGGGGAAAGCGCGCGGT	308
Db	564	---AAGCAGCAAGAGGGCTCAGGGGAAGGCGTCCCGCTCGGCGGGGGA---CGCTGGC	617
OY	309	GCAGCGCGGGGACACGGCCTCGGG---CTGGCACCTGGCTGTAGGGAATGTCGTCTGGA	364
Db	618	TCAGGTGTGGGACACGCACTGTGACTGTGCACTGGCACCTGGAGATGTCCGCTCGGC	677
OY	365	TAAAGTGGCAGTGGACCCGCGCATATGGCGGGGCTCTGGGGGCTTCTGCTGGCTGGTGGGGCT	424
Db	678	CGAGGTGCATGAGACCCGCGCATATGGCGGGGCTCTGGGGGCTTATGCTGTGGTCTTGGGCT	737
OY	425	TCGTGAGGGGCGGCTTTCGCTGTGCCCATCGTCTTGCAATGCGAGTCCCTTCGTGATCTGGT	484
Db	738	TCGTGAGGGGCTTCTCTTCTGCTCGCCCATGTCTGTCAAAATGCGACCACTGTAGATTGGT	797
OY	485	GCAGGAGCCCTTCTCTCGGGCATATCGTGGGATTTCCGAGTTGGAGCCCTTAACGTATATC	544
Db	798	GTACCGAGCCCTTCTCTCGGCATATCGTGGATTTCCGAGTTGGAACTTAACGACATTAACC	857
OY	545	CTGAGAACATCAACCGAAATTTTTCATATCGCAACACGAAAGAGTTGAAATCATCAACAGAG	604
Db	858	CAGAGAACATCAACCGAAATTTCTATATGCAACCGAAAGAGTTGAAATCATCAATGAG	917
OY	605	ATGATGTGGAAGCTTATATGTGGACCTGAGAAATCTGCACATTTGTGATTTCTGGATTAAT	664
Db	918	ATGATGTGGAAGCTTACGTGGGGGCTGAAAACTTTCACATATGTGATTTCCGGCTTAAAGT	977
OY	665	TTGATGGCTCATTAAGCATTTCTGAAAAACACAACTGTGACACATCAATTTTACCCGAA	724
Db	978	TTGTGGCTTTCAAAGCGCTTCTGTAAAGAACGGCACCTGGCGCATCAATTTTCACTCGAA	1037
OY	725	ACAAACTGACGAGTTTGTCTAGAAACATTTCCGTCACCTTGACTTGTCTGAACTGATCC	784
Db	1038	ACAACTGACGAGTTTGTCTAGAGAACATTTCCGCGACCTTGACTTGTCTGACTGATCC	1097
OY	785	TGGTGGGGAATCCATTTACATGCTCCCTGTGCATTAATGTGATCAAGACTTCCAAAGG	844
Db	1098	TGACGGGTAAATCCGTTACGATGCTGTGTGACATCATATGTGGCTCAAGACTTCCAGAGA	1157
OY	845	CTAAATCCAGTCCAGACACTGAGATTTGTACTGCTGTGAATGAAGACGACAAATATTC	904
Db	1158	CGAATTCAGGCCCGGACACTCAGGATTTGTATTTGCTCTCAATGAGAGCGACGAAATACC	1217
OY	905	CCCTGGCAAACCTGCGAATACCCCAATTTGTGTTGGCATCTTGCAATCTGGCGCGACCTTA	964
Db	1218	CTCTGGCAAACCTGCGAATTTCCCAATTTGTGTCTGGCCCTGTGCACGTCTGGCCCTCTTA	1277
OY	965	ACCTCACTGTGGAGGAAGAAAGTCTATCACTATACCTGTAGTGGCAGGTATCCGG	1024
Db	1278	ACCTCACTGTGGAGGAAGGAAGTCTGTGACCATTTCTTGCAAGGTGGGGGGTAACTGGC	1337
OY	1025	TTCTTAATATGTATTGGAGATTTGGTAACTGTGTTCCAAATATATGAAATGAACAAGCC	1084
Db	1338	TTCCCACTTGTATCTGGGACGTTGGGAATTTGGTTTCAAAACATGAAATGAACAAGCC	1397
OY	1085	ACACACAGGGCTCCTTAAGATTAATTAATTTTCATCGATGACATGTGGGAAGCAATCT	1144
Db	1398	ACACACAGGGCTCCTTAAGATTAACAAATTTTCATCGAATGACATGTGGGAACAAATCT	1457
OY	1145	CTTGTGTGGCGGAAATCTTGTAGAGAGAATCAAGATTTCTGTCAACCTCACTGTGCAT	1204
Db	1458	CTTGTGTGGCGGAAACCTCGTGGAGAAAGATCAAGACTCTGTGAACCTCACTGTGCAT	1517
OY	1205	TTGCACCACTATCACTTTTCTCGAATTTCCAACTTCAGACCACTGTGTGATTCAT	1264
Db	1518	TTGCACCACTATCACTTTCTCGAATTTCCAACTTCAGACCACTGTGTGATTCAT	1577

QY	1265	TCACCTGTGAAGGCAACCCCAACCAAGGCTTCAGTGGTCTTATATACGGGGCAATTGGA	1324
Db	1578	TCACCTGTGAAGGCAACCCCAAGCCAGACATTCAGTGGTCTTATACAAAGGACATCTGA	1637
QY	1325	ATGAGTCCAAATPACATCTGTACTATAAATACATGTTACCAATACACAGAGTACCAAGCT	1384
Db	1638	ATGAGTCCAAAGTACATCTGTACCAAAATACGTCAACCATACACAGAGTACCAAGCT	1697
QY	1385	GCCTTCAGCTGGATTAATCCCATCTACATGAACAATGGGGACTACACTTAATAGCCAGA	1444
Db	1698	GCCTTCAGCTGGATTAATCCCATCTCATATGAATATAGAGACTACACCTTAATAGCCAGA	1757
QY	1445	ATGAGTATGGGAAGGATGAGAAACGATTTCTGTCTCATCTTCAATGGGCTGGCTGGAATTG	1504
Db	1758	ATGATATATGGGAAGGACAGAGACAGATTTCTGTCTCATCTTCAATGGGCTGGGAGTTTG	1817
QY	1505	ACGATGTGGCAAAACCCAAATTATCCTGATGTAAATTATGAACATTATGGAATGACGACCGA	1564
Db	1818	ACTATGAGACAAACCCAAATTATCCTGAAAGTCTCTATGAAAGCT---GACCAAGCCAA	1874
QY	1565	ATGACATCGGGGACACCAAGAACAGAAATGAAATCCCTTTCACAGACGTCACTGATA	1624
Db	1875	CTGACATCGGGGATACCTAACAAAGAAATGAGATCCCTTCACAGAGTGTGTGACCC	1934
QY	1625	AAACCGGTGGGACATCTCTGTGTCTATGTGTGTGTGATTTGGCTCTGTGTGGGAT	1684
Db	1935	AAACCAATCGGGAGCATCTCTGTGTCTATGTGTGTGTGATTTGGCTCTGTGTGGGAT	1994
QY	1685	TTTGGCTTTTGGTATGTGCTGTTTCTGCTTAAGTGGCAAGACATCCAAAGTTTGGCATGA	1744
Db	1995	TTGTGCTGTGGTGTGTGCTGCTTCTGTCTCAAGTGGCAGAACATTCAAAGTTTGGCATGA	2054
QY	1745	AAGGCCAGCCTCCGTTATACAGCAATGATGACTCTGCGACGCCATCTCATCATCT	1804
Db	2055	AAAGGCCAGCTTCCGTCATACAGCAACGACATGACTGTGCGACGCCCTCTCCACCAATCT	2114
QY	1805	CCAATGGAGATACATCTCCATCTTCTTGGAAAGTGGCCCAAGTGTGTATATTGGA	1864
Db	2115	CCAAGGGAGACACATCCGTCCTTCTTGGAGGGCGGCGCCGATGTGTATCATATTGGGA	2174
QY	1865	TGACCAAAATCCCTGTCAATTGAAATCCCACTTACTTTTGGCATCACCAACATGCACTCA	1924
Db	2175	TGACCAAAATCCCTGTCAATTGAAACCCCACTTACTTGGTATCACCAACATGCACTCA	2234
QY	1925	AGCCGACACATTTGTTGACGACATCAAGCGACATTAATTTCTGAAAGGGAAGCTAG	1984
Db	2235	AGCCGACACATTTGTTGACGACATCAAGAGACACAACTCGTTCTGAAAGGGAAGCTTG	2294
QY	1985	GGAAAGAGCCTTTGAAAAGTGTCTTAGCTGAATGTATTAACCTGTGTCTGAGCAGG	2044
Db	2295	GAGAAAGAGCCTTTGGAAGATTTTCTTAGCGGAGGTATTAACCTGTGCCCGAGCAAGG	2354
QY	2045	ACAAATCTTGTGTGGCAGTGAAGACCCCTGAAGAGATGCCATGACAAATGCAACGCAAGACT	2104
Db	2355	ATTAATCTTGTGTGGCCGTGAAGAGCTGAAGAGAGCGCCAGCAAAATGCTCGCAAGACT	2414
QY	2105	TCCACCGTGAAGCCGAGCTCCTGACCAACCTCAGAGATGAGACATGTCAAAGTTCTATG	2164
Db	2415	TTCAATCGGAAGCCGAGCTGCTGACCAACCTCAGAGCAAGACATTTGCAAGTTCTTAG	2474
QY	2165	GGCTGTGGGTGAGGGGCGACCCCTCATATCATGATGATCTTTAGTATGATGAAGCATGGGAC	2224
Db	2475	GGTCTGTGTGGAAGGGGCGACCACTCATATCATATGATCTTTAGTATCATGAAGCAAGGGAC	2534
QY	2225	TCACCAAGTTCTCTCAGGGGACACGGGCTGATGCCGTGATGCTGAGGGGCAACCCGC	2284
Db	2535	TCACCAAGTTCTCTTAGGGGACACGGGCGAGATGCGATGCTGATGGGAGGGATACCCGC	2594
QY	2285	CCACGGAACTGACGAGTCCGAGATGTGCAATATGCGCAGAGCATTCGGCCGGGGATGG	2344
Db	2595	CCACGGAGCTGACGAGTCCGAGATGTGCAATATGCTCAGCAAAATCGCAGCGAGATGG	2654
QY	2345	TCACCTGTGGCGTCCAGCATCTTGTGACCGGCAATTTGGCCACCAAGAACTGCGCTGTG	2404


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Db 2655 TCTACCTGGCACTCCCAACATCTTGCAACCGAGCCTGGCCACCAGCACTTGAG 2714
Qy 2405 GGGAGAACTTGCTGATGAAAATCGGGGACTTGGGATGTCCGGGAGCTGACGACTG 2464
Db 2715 GAGGAACTCTCTGTGAAAATTTGGGACTTGGGATGTCCGGGATGTATACGACCG 2774
Qy 2465 ACTACTACAGGGTGGTGGCCACAACAATGCTGCCATTCGTGATGCTTCAGAGCA 2524
Db 2775 ACTACTACGGGTTGGTGGCCACAACAATGCTGCCATTCGTGATGCTTCAGAGCA 2834
Qy 2525 TCATGTACAGAAATTCACGACGGAAGCAGCTGTGAGCCTGGGGTCTGTGTGG 2584
Db 2835 TCATGTACAGAAATTCACGACGGAAGCAGCTGTGAGCCTGGGGTCTGTGTGG 2894
Qy 2885 AGATTTTCACTATGAGGAAAGCCGTGTACGAGCTGTCAACAAATGAGGTATAGT 2644
Db 2895 AGATTTTCACTATGAGGAAAGCCGTGTATCGCTATCAACAAAGGTATAGT 2954
Qy 2645 GTATCACTCAGGGCCGAGTCTTGACGACCCCGCAGCTGCCAGAGGTTGATGAGC 2704
Db 2955 GCATCACTCAGGGCCGAGTCTTGACGACCCCGCAGCTGCCAGAGGTTGATGAGC 3014
Qy 2705 TGATGCTGGGGTGTGCGAGCGAGAGCCCAATGAGAGAAACATCAAGGCAATCATA 2764
Db 3015 TGATGCTGGGGTGTGCGAGCGAGAGCCCAATGAGAGAAACATCAAGGCAATCATA 3074
Qy 2765 CCCCTCTTCAAGAACTTGCGCCAAAGCATCTCGGTCTACCTGTGACATTTAGCTAG- GGC 2823
Db 3075 CACTCTTCAAGAACTTGCGCCAAAGCATCTCGGTCTACCTGTGACATTTAGCTAGCTC 3134
Qy 2824 CCTTTTCCCCAGACCGATCTTCCCAAGTACTCTCAGAGGGGTGAGAGTAAACAT 2883
Db 3135 CCTCTCTCCCAAGACCGCTTCCCAAGCAACCTCTGAC----- 3175
Qy 2884 CTTTAACTGCGCTGAGGCGCACCAAGCTCTCTCTTCACTGTGACAGTATTAACATC 2943
Db 3176 CTTTAACTGCGCTGAGGCGCACCAAGCTCTCTCTCTGAGAGTATTAACATC-- 3232
Qy 2944 AAAAGTCCGGAAGCTCTGAGGGAAGCAATGTGATTTTCACTCATAGACAGTA 3003
Db 3233 AGACAAAGAGCGCTCTCCGGGAGGAGCAATGCGCACTTCCCATTCACAG--ACAGTA 3290
Qy 3004 TTGACTCTTTTGGCATTAATCTCTCTC----- 3035
Db 3291 TCGACTCGCTTGGCTTGTGCTTCTCTCTCTGCTTGGTGTCTTTTGGCCCA 3350
Qy 3036 -----TTTCAATCTCCCTGGTGTCTCTTTCTT 3067
Db 3351 TTTCATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 3410
Qy 3068 TTTTAAATTTCTTTTCTTCTTTTGTGCTTCCCTGCTTCAAGTCTTACCTT 3127
Db 3411 CTATCTATCTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 3470
Qy 3128 CTTTGAATCAATGCGCTTCTGATTAATTAATCTGATTAAGCAAGGCTTACA 3187
Db 3471 CTCTTGACGATCGCTTCTGATCTTAATTAATCTGATTAAGCAAGGCTTACA 3550
Qy 3188 AACGTAATTTGTTATATGAGACACTCAGTTTGCACACAACTAATAGCTTG 3247
Db 3551 AACGTAATTTGTTATATGAGACACTCAGTTTGCACACAACTAATAGCTTG 3590
Qy 3248 TTGTAATCTGCTTGTGATGTGATGAAAAAAGGAAAAACAATATTT--TCAGTT 3301
Db 3591 TTGTAATCTGCTTGTGATGTGATGAAAAAAGGAAAAACAATATTTGATC 3650
Qy 3302 AAACCTTGTCACTCTGTGATGATGAGATTTCTATGATTAATCTTATTTAT 3361
Db 3651 TTAAACCTGTCACTCTGTGATGATGAGATTTCTATGATTAATCTTATTTAT 3710
Qy 3362 TTAT-----TATTTATCTGTTCTTATTTGTTTGTGATGAGCTTAAAG 3402
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Db 3711 CTATTTATTTATTTATTTATTTATTTATTTCTCTTCTTGTGTTTCCGCTGTTAG 3770
Qy 3403 CCTGTGTATATAAAGAACTTGTTTCAATCTGTGAAGCTTTATCTATGAGATTA 3462
Db 3771 CTTGTGTATGAAAGAAAGTATGATGAGTCTGGGAAAACTTATCTGTGGGAAATG 3830
Qy 3463 AAACGAA--GAGAAAGAAATTTATTAAGACCGCAATGTGGAGAAACAAGAAC 3520
Db 3831 AAACGAAAGGGGAAAGAACTTTACATTAAGCAGCAGAGATGAGACAGAAAAAGC 3890
Qy 3521 ACTGGATCAGCTGTGCTGATCCCTACTTAAAGAAATCTCAGAACTGTAGCTGGAA 3580
Db 3891 CATTGATCAGCCAGATCTGCTGAT--AGAAAAACCGAGCATCAGGCTGAG 3948
Qy 3581 GAATGTATCGGCACTTCCCTGAGAGACCTTCTGAGAGTAAAGAACTAGGCTC 3640
Db 3949 GATCATTTGGGCACTGACCCCGAGAGACCTTTCTGAGAGACAGAAATTTAACTC 4008
Qy 3641 TGTGCAATGGA 3651
Db 4009 TGCATCATGGA 4019

RESULT 15
ADRI5010
ID ADRI5010 standard; DNA; 4757 BP.
AC ADRI5010;
XX 21-OCT-2004 (first entry)
XX
XX Rat electroconvulsive seizure (EC) signature gene seqid 43.
DE
XX neuroleptic; nootropic; antidepressant; eating disorder; tranquilizer;
XX neuropsychiatric disorder; signature gene; electroconvulsive seizure;
XX EDS; schizophrenia; autism; major depressive disorder; MDD;
XX bipolar affective disorder; BAD; psychotic depression; anxiety disorder;
XX eating disorder; attention deficit hyperactivity disorder;
XX neuropsychiatric drug; gene; ss; rat.
XX
XX Rattus norvegicus.
OS
XX
XX US2004152107-A1.
XX
XX 05-AUG-2004.
XX
XX 18-SEP-2003; 2003US-00664705.
XX
XX 18-SEP-2002; 2002US-0411718P.
XX 09-DEC-2002; 2002US-0411882P.
XX 18-JUN-2003; 2003US-0479970P.
XX
XX (ALTA/) ALTAR C. A.
XX (LAEN/) LAENG P.
XX (YOUN/) YOUNG T. A.
XX (CHAR/) CHARLES V. D.
XX
XX Altar CA, Laeng P, Young TA, Charles VD;
XX
XX WPI; 2004-580183/56.
XX
XX Identifying compound to treat neuropsychiatric disorder, by contacting
XX cell, with test compound, determining expression of signature genes by
XX cell, comparing expression of signature genes to expression in cell not
XX contacted with compound.
XX
XX Claim 1; SEQ ID NO 43; 186bp; English.
XX
XX The invention describes a method of identifying (M1) a compound to treat
XX a neuropsychiatric disorder. The method involves contacting a cell with a
XX test compound, determining the expression of one or more signature genes
XX by the cell, each signature gene comprising a nucleic acid that
XX hybridizes to a nucleic acid chosen from 154 fully defined sequences (S1)
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CC of e.g., 4154, 1582, 645, 367, 405, 1080, 580, 1159, 539, 465, 2002,
CC 2469, 3155, 421, 2957, 644, 2562, 2858, 1194 and 1227 base pairs as given
CC in the specification and their complements, and comparing determined
CC expression of one or more signature genes to expression in cell not
CC contacted with test compound. Also described are: selecting (M2) one or
CC more signature genes that are indicative of an effective therapy for
CC treating a neuropsychiatric disorder; and a kit (I) for detecting an
CC electroconvulsive seizure (ECS) gene signature, comprising several
CC oligonucleotides, each of which is capable of specifically hybridizing to
CC a different ECS signature gene. Therapeutic methods, which use ECS gene
CC signatures and ECS signature genes to treat, ameliorate or prevent
CC neuropsychiatric disorders, is also disclosed. (M1) is useful for
CC identifying a compound to treat a neuropsychiatric disorder chosen from
CC schizophrenia, autism, major depressive disorder (MDD), bipolar affective
CC disorder (BAD) and psychotic depression. (M1) is useful for identifying
CC compounds for treating neuropsychiatric disorders such as anxiety
CC disorders, eating disorders and attention deficit hyperactivity disorder.
CC The ECS signature genes of (M1) are useful in diagnostic and prognostic
CC methods of identifying people who have or who are susceptible to
CC neuropsychiatric disorders such as MDD and BAD. (M1) enables multi-
CC parameter high throughput screening of compounds for treating
CC neuropsychiatric disorders; screening of large number of candidate
CC compounds for treating neuropsychiatric disorder and enables cost-
CC effective and rapid screening of compounds useful as neuropsychiatric
CC drugs. This sequence represents an electroconvulsive seizure (ECS)
CC signature gene.

XX Sequence 4757 BP; 1122 A; 1288 C; 1197 G; 1150 T; 0 U; 0 other;

Query Match 61.1%; Score 2264.2; DB 13; Length 4757;

Best Local Similarity 79.5%; Pred. No. 0; Mismatches 618; Indels 134; Gaps 15;

Matches 2919; Conservative 0; Mismatches 618; Indels 134; Gaps 15;

QY 74 GGGCGCATGACGACGAGCGCGCGCGAGCTCCGACGAGCGGTAGCGCCCTGTAAAGC 133
DB 390 GAGCCACCGAGTGGCGCGCTGGCGTATAGAACCATGACCGCGCTTGTGGCTTGAGAGACG 449
QY 134 GGTTCGCTATGCGGAGACCACTGTGAACCTGCGCGCTCCGGAACACTTTCGCTC--- 190
DB 450 GGGCGGTGATGTTCCAGCCCACTGTGAACCATTTGTGTACGCGCCCAACTGCTCAGCGCCAG 509
QY 191 --GGGACAGCTGACGCTCTGTATAGCTGACCTGGGACGCGCGGCAACAAGACCGAGGA 248
DB 510 CACCGACAGGCTCAGCCTCTGTATAGCTCTCTCTGGCGGAGCGCATCAGACAC----- 563
QY 249 GTTAAAGAGACCGGACGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 308
DB 564 ---AAGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 617
QY 309 GCAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 364
DB 618 TCAGCGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 677
QY 365 TAAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 424
DB 678 CAGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 737
QY 425 TCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 484
DB 738 TCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 797
QY 485 GCAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 544
DB 798 GTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 857
QY 545 CTGAG 604
DB 858 CAGAG 917
QY 605 ATGATGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 664
DB 918 ATGATGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 977

QY 665 TTGTGCTGATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 724
DB 978 TTGTGCTGATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1037
QY 725 ACAAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 784
DB 1038 ACAAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1097
QY 785 TGTGAG 844
DB 1098 TGACGGGATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1157
QY 845 CTAAATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 904
DB 1158 CGAAATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1217
QY 905 CCTGAG 964
DB 1218 CTGTGAG 1277
QY 965 ACCTGAG 1024
DB 1278 ACCTGAG 1337
QY 1025 TTCTTAATATGATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1084
DB 1338 TCCCACTTGTATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1397
QY 1085 ACACAGAG 1144
DB 1398 ACACAGAG 1457
QY 1145 CTGTGTGAG 1204
DB 1458 CTGTGTGAG 1517
QY 1205 TTGACCAATATATCAATTTCTGAAATCTTCGAACCTTCAGACCACTGAGTGCATTCAT 1264
DB 1518 TTGACCAATATATCAATTTCTGAAATCTTCGAACCTTCAGACCACTGAGTGCATTCAT 1577
QY 1265 TCACTGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1324
DB 1578 TCACTGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1637
QY 1325 ATGAGTCCAAATATCATCTGTATTAAT 1384
DB 1638 ATGAGTCCAAATATCATCTGTATTAAT 1697
QY 1385 GCTTCCAGCTGATTAATCCATCTCAATGAACCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1444
DB 1698 GCTTCCAGCTGATTAATCCATCTCAATGAACCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1757
QY 1445 ATGAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1504
DB 1758 ATGAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1817
QY 1505 ACGATGAG 1564
DB 1818 ACGATGAG 1874
QY 1565 ATGACATCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1624
DB 1875 ATGACATCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1934
QY 1625 AAACCGGTGAG 1684
DB 1935 AAACCGGTGAG 1994
QY 1685 TTGAGCTTTGATATGCTGTTCTGCTTAAGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1744
DB 1995 TCTGCTGCTGATGATGCTGCTTCTGCTCAAGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2054
QY 1745 AAGGCCAGGCTTCGTTATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1804

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Db 2055 AAGGCCAGCTTCGCTATGAGCAAGAGATGACTTCGCAAGCCCTCTCCACACATCT 2114
Qy 1805 CCAATGGAGATGATACCTCATCTTCTTGGAAAGGCGCCAGATGCTGTATTTGGA 1864
Db 2115 CCAAGGGAGACACTCTCTTCTTGGAGGGGGGCCGAGTGTCTATCATTTGGGA 2174
Qy 1865 TGACCAAGATCCCTGTCAATTGAAATCCCACTTCTTGGATCAACCAAGTCACTCA 1924
Db 2175 TGACCAAGATCCCTGTCAATTGAAATCCCACTTCTTGGATCAACCAAGTCACTCA 2234
Qy 1925 AGCCAGACACTTTTGTGACATCAAGGACATTAATTTGTGAAAAGGAGCTAG 1984
Db 2235 AGCCAGACACTTTTGTGACATCAAGGACATTAATTTGTGAAAAGGAGCTAG 2294
Qy 1985 GCGAAGGAGCTTTGSAAGATGTTCTAGCTGAATGTATTAACCTCTGCTGAGCAG 2044
Db 2295 GAGAAAGGAGCTTTGSAAGATGTTCTAGCTGAATGTATTAACCTCTGCTGAGCAG 2354
Qy 2045 ACAAGATCTTGTGGAGTGAAGACCTTGAAGATGCGATGACATGCAAGCAAGACT 2104
Db 2355 ATAAGATCTGTGGCGGTGAAGAGCTGAAGAGCGCAGAGCAATGCTGCAAGACT 2414
Qy 2105 TCCACCGTGAAGCGAGCTCTGTACCAACTCTCAGCATGACACATGCTCAAGTTCTAG 2164
Db 2415 TTTATCGGAAAGCGAGCTGTCTGACCAACTCTCAGCAGACACATGCTCAAGTTCTAG 2474
Qy 2165 GCGTCTGTGAGGAGGCGACCCCTCATCATGCTTGTGATACATGAAGATGGAGCC 2224
Db 2475 GTGTCTGTGAGGAGGCGACCCCTCATCATGCTTGTGATACATGAAGATGGAGCC 2534
Qy 2225 TCAACAAGTTCTCTAGGCGACACAGGCGCTGATGCGTCTGATGGCTGAGGCAACCCGC 2284
Db 2535 TCAACAAGTTCTCTAGGCGACACAGGCGCGAATGCAAGTCTGATGGCAGAGGTAACCCGC 2594
Qy 2285 CCACGGAATGACGAGTGCAGATGCTGATATATAGCCACAGCATGCGCGGCGATGG 2344
Db 2595 CCACGAGCTGACCGCAGTGCAGATGCTGACATGCTCAGCAATGCGCAGCAGCATGG 2654
Qy 2345 TCTACCTGCGCTCCACAGACTTGTGACACCGCATTTGGCCACAGAACTGCTGTGCG 2404
Db 2655 TCTACCTGCGCATCCCAACACTTGTGACACCGCATTTGGCCACCGAACTGCTGTGAG 2714
Qy 2405 GGGAGAAGTTCTGTGTAATCGGGGACTTTGGGATGTCCGGGAGCTGTACAGCACTG 2464
Db 2715 GAGGAAGCTGTGTGTAATCGGGGACTTTGGGATGTCCGGGATGTGTACAGCACTG 2774
Qy 2465 ACTACTACAGGATCGTGGCCACAATGCTGCCATTTGCTGATGCTTCAGAGAGCA 2524
Db 2775 ACTACTACAGGATCGTGGCCACAATGCTGCCATTTGCTGATGCTTCAGAGAGCA 2834
Qy 2525 TCAATGTACAGAAATTCACAGCGAAAGCAGCTGTGAGCTGTGGGGTCTGTGTTGGG 2584
Db 2835 TCAATGTACAGAAATTCACAGCGAAAGCAGCTGTGAGCTGTGGGGTCTGTGTTGGG 2894
Qy 2585 AGATTTTCACTATGAGCAAGCCCTGTGTACAGCTGTCAAACAATGAGGTATAGT 2644
Db 2895 AGATTTTCACTATGAGCAAGCCCTGTGTATCAAGCTATCAACCAAGGATGATAGT 2954
Qy 2645 GTATCACTCAGGCGAGTCTGTGACGACCCCGCAGCTGCCCCAGAGGTTATAGC 2704
Db 2955 GCATCACCGGAGGAGAGTCTTTCAGGGGCTCGAGGTGTCCCAAGAGGTTATAGC 3014
Qy 2705 TGATGCTGGGTTGCTGGCAGCGAAGACCCCACTAGAGAAATCAAGGCACTCA 2764
Db 3015 TGATGCTGGGATGTGGCAGCGGAAACCAACAGAGAAATCAAGGCACTCA 3074
Qy 2765 CCTCTCTTCAAGAACTTGGCCAAAGGATCTCGGTCTACTGACATTTAGGCTAG--GGC 2823
Db 3075 CACTCTTTCAAGAACTTGGCCAAAGGAGTGTCCGCTTACTGACATTTAGGCTAGCTC 3134
Qy 2824 CTTTTCCTCCAGACGATCTTCCCAAGTACTCTCAGACGGGCTGAGAGATGAACAT 2883

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Db 3135 CTTCTTCTCCAGAGCGGCTTCCCAAGCACCCCTCAGAC----- 3175
Qy 2884 CTTTAACTGCGCGCTGGAGGCGACCAAGCTCTCTCTTCACTGTGACAGATTAACATC 2943
Db 3176 CTTTAACTGCGCT--GATGACACCACTTCTCTCTCTGCTGTGACAGTGTAA-- 3232
Qy 2944 AAAGACTCCGAAAGCTCTGAGGAAAGCAGTGTATCTTTGATCCATGACACAGTA 3003
Db 3233 AGACAAAGAGGCGCTCTCCGGGTGAGGACAGTGGCACTTCCCATCCAG--ACAGTA 3290
Qy 3004 TTGACTCTTTTGGCATATCTCTTCTC----- 3035
Db 3291 TCGACTGCTTGGCTTGTGTGCTCTCCCTTGTGTGTCTTTCTTTGCCCA 3350
Qy 3036 -----TTTCATCTCCCTGGTGTCTCTTTCTTT 3067
Db 3351 TTTCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3410
Qy 3068 TTTTAAATTTTCTTTTCTTTTCTTTTCTTTTCTTTCTTTCTTTCTTTCTTTCTTT 3127
Db 3411 CTATCTATCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3470
Qy 3128 CTTTGAATCAATCTGCTTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTA 3187
Db 3471 CTCTTGAACGATCTGCTTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTA 3530
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Qy 3641 TGTGCATGGA 3651
Db 4009 TGCATGATGGA 4019

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Search completed: February 18, 2005, 12:26:58
 Job time : 2106.06 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 01:09:31 ; Search time 12944.8 Seconds
(without alignments)
10900.495 Million cell updates/sec

Title: US-10-645-546-1

Perfect score: 1 ccccccattcgcatctaacaa.....gtagagagcaaatgagcttc 3707

Sequence: IDENTITY NUC

Scoring table: Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1643.2	44.3	3092	3	BC075804 Homo sapi
2	1134.6	30.6	2375	3	AK018789 Mus muscu
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5	833.4	22.5	996	7	CN802365 IL10M1G8N
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20	576.8	15.6	644	6	CB450137 704769 MA
21	569.4	15.4	582	4	BP446867 BP446867
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27	550.8	14.9	801	7	CF746341 UI-M-GV0-
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35	513.2	13.8	574	4	BI682385 463453 MA
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37	511	13.8	2179	9	AY419091 Homo sapi
38	500.2	13.5	680	5	BP112935 BP112935
39	498	13.4	644	4	BM491989 ppg2n.p0
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41	495.6	13.4	2515	3	CR625585 full-1leg
42	490.2	13.2	644	7	CF746162 UI-M-GV0-
43	488.8	13.2	706	5	BX913744 BX913744
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45	487	13.1	655	6	CD769219 AGENCOURT

ALIGNMENTS

RESULT 1	BC075804	Homo sapiens cDNA clone IMAGE:4939307, with apparent retained intron.	3092 bp	mRNA	linear	HTC 19-JUL-2004
ACCESSION	BC075804	GI:50368967				
VERSION	BC075804.1					
KEYWORDS	HTC					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1	(bases 1 to 3092)				
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Butow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Udell, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Kitzwinkl, M.J., Skalska, U., Smalls, D.E., Scherch, A., Schein, J.B., Jones, S.J. and Marra, M.A.					
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences					
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	99	(26)			16899-16903 (2002)
PUBMED	12477932					
REFERENCE	2	(bases 1 to 3092)				
AUTHORS	Strausberg, R.					
TITLE	Direct Submission					
JOURNAL	Submitted (06-JUL-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA					
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov					
COMMENT	Contact: MGC help desk Email: cgabbs-remail.nih.gov Tissue Procurement: David N. Louis, M.D. cDNA Library Preparation: Life Technologies, Inc.					

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcdpaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAX Plate: 166 Row: f Column: 18
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 21361305
This clone has the following problem: retained intron.

FEATURES

SOURCE

1. 3092
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4939307"
/tissue_type="Brain, anaplastic oligodendroglioma with
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/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 44.3%; Score 1643.2; DB 3; Length 3092;
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Matches 1706; Conservative 0; Mismatches 3; Indels 41; Gaps 2;

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Qy 1319 TATTAATGAGTCCAAATTAATCTGTACTAAATATCAATGATGATGATGATGATGATGAT 1378
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RESULT 2
AKO18789
LOCUS
DEFINITION
2375 bp mRNA linear HTC 03-APR-2004
Mus musculus adult male cerebellum cDNA, RIKEN full-length enriched library, clone:1500040113 product:DJ245M18.1 (PLACENTAL PROTEIN DIFP40) (FRAGMENT) homolog [Homo sapiens], full insert sequence.

ACCESSION
AKO18789
VERSION
AKO18789.1 GI:12858688
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
Carninci, P. and Hayashizaki, Y.
TITLE
High-efficiency full-length cDNA cloning
JOURNAL
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE
99279253
PUBMED
10349636

REFERENCE
AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL
Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE
20499374
PUBMED
11042159

REFERENCE
AUTHORS
Shibata, K., Itoh, M., Aizawa, K., Nagasaka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, U., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL
Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE
20530913
PUBMED
11076861

REFERENCE
AUTHORS
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE
Functional annotation of a full-length mouse cDNA collection
JOURNAL
Nature 409, 685-690 (2001)
MEDLINE
11076861
PUBMED
11076861

REFERENCE
AUTHORS
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL
Nature 420, 563-573 (2002)
MEDLINE
11076861
PUBMED
11076861

REFERENCE
AUTHORS
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Aizawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kankawa, T., Kato, H., Kawai, J., Kojima, Y., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Teijima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
TITLE
Direct Submission
JOURNAL
Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome

COMMENT
Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.jp/) for further details.

FEATURES
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1. .2375
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/mol_type="mRNA"
/strain="C57BL/6J"
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ORIGIN
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polyA_site
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Best Local Similarity 82.3%; Pred. No. 5.4e-278;
Matches 1383; Conservative 0; Mismatches 274; Indels 24; Gaps 6;
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 Db 816 AGTTGAAGCTTATGTTGAGAACTGCAATTTGATTTGATTTAAATTTG 875
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 Qy 788 TGGGCAATTCATTTACATGCTCTGATGATTTGATTTGATTTGATTTG 847
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 Qy 848 AATCAAGTCAAGCACTGAGATTTGATTTGCTGCAATTTGATTTGATTTG 907
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 Qy 908 TGGGCAATTCATTTACATGCTCTGATGATTTGATTTGATTTGATTTG 967
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 Qy 968 TCACTGAGAGAAAGTCTATCAATTTGATTTGATTTGATTTGATTTG 1027
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 Qy 1028 TCAATATGATTTGAGATTTGATTTGATTTGATTTGATTTGATTTG 1087
 Db 1236 TCAATATGATTTGAGATTTGATTTGATTTGATTTGATTTGATTTG 1295
 Qy 1088 CACAGGCTCTTAAAGATTAATCAATTTGATTTGATTTGATTTGATTTG 1147
 Db 1296 CACAGGCTCTTAAAGATTAATCAATTTGATTTGATTTGATTTGATTTG 1355
 Qy 1148 GTGAGGGAAGAAATCTTGAAGAGATCAAGATTTGATTTGATTTGATTTG 1207
 Db 1356 GTGAGGGAAGAAATCTTGAAGAGATCAAGATTTGATTTGATTTGATTTG 1415
 Qy 1208 CACCAATATCAATTTCTGATTTGATTTGATTTGATTTGATTTGATTTG 1267
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Qy 1388 TCCAGCTGATTAATCCCACTCACTGAACAAATGGGACTCACTTAATAGCCAAAGATG 1447
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 Db 1833 GCAATGGGGAACCAATCTGCTGATTAATTTGATTTGATTTGATTTGATTTGATTTG 1892
 Qy 1688 GCGTTTGTATGATGCTGTTTCTGCTTAAGTTGGCAAGCACTCCAACTTTGGCATGAAG 1747
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 Qy 1748 G 1748
 Db 1953 G 1953

RESULT 3
 AK028827
 LOCUS
 DEFINITION
 Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:473246C10 product:DJ245M18.1 (PLACENTAL PROTEIN D1P40) (FRAGMENT) homolog [Homo sapiens], full insert sequence.
 ACCESSION
 AK028827
 VERSION
 AK028827.1 GI:26081044
 KEYWORDS
 HTC; CAP trapper.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 JOURNAL
 MEDLINE
 PUBMED
 20499374
 11042159
 REFERENCE
 AUTHORS
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kikunishi, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsubara, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 JOURNAL
 MEDLINE
 PUBMED
 20530913
 11076861
 REFERENCE
 AUTHORS
 4
 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
AUTHORS 6 (bases 1 to 2285)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Niehi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.
FEATURES
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ORIGIN
misc_feature
Query Match 30.6%; Score 1133; DB 3; Length 2285;
Best Local Similarity 81.6%; Pred. No. 1,4e-277;
Matches 1391; Conservative 0; Mismatches 290; Indels 24; Gaps 6;
QY 77 CCATGACAGCAGCGCGCGCGAGCTCCGAGCAGCGGTAGCGCCCTCTTAAAGCGGT 136
DB 210 CCACCGAGTGTGCTCTGCGTATAGACTATGACACCGCCTTGTGGCTCGAGAGCGGGC 269
QY 137 TCGCTATGCCGGGACCACTGTGAACCTGCGCGCTGCGGAACTCTTTCGTC-----C 191
DB 270 CCGGATATCCACGACCTGTGMAACATTGGTGTGCGCCCAACTGTCTACGCCCCAGAC 329
QY 192 GGACCACTCAAGCTCTGATAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 251
DB 330 CGACAGGCTCAAGCTCTGTAGTCTCACTCGCGGGAG-GCCACACAGACCAAGACACA 388
QY 252 AAGAGAGCCGCAAGGCGAGGAGGCTCTCCCGCAGCGGCTGGGGGAGGAGGCGCGGTGCA 311
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QY 312 GCGCGGACACAGGCACT-----CGGCTGGCACTGGCTGAGGAGATGCTCTGAGATTA 367
DB 438 GGTAGAGGACACGCACTCCGACTAGTGGCACTGGAGCTGGGAGATGCTGGCTGGCTGCA 497
QY 368 GGTGGCATGACCCCGCAGTGGCGGCGCTTGGGGCTTCTGCTGGCTGGTGTGGCTTCT 427
DB 498 AGTGGCATGACCCCGCAGTGGCGGCGCTTGGGGCTTATGCTGCTGCTTGGGGCTTCT 557
QY 428 GGAGGGCGCGTTTGGCGCTGCCAGTCTGCAATATGAGAGCTCTGGATTCGGTGA 487
DB 558 GGAGGGCGCTTCTGCGCTGCCAGTCTGCAATATGAGAGTTCGCTAGATTTAGTGA 617
QY 488 GCGACCTTCTCTGGCATCTGGCATTTCCGAGATTGAGACCTTAACAGTATGATCTGG 547
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DB 1458 AGTCCAAATATCATCTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1517

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Db	1518	TTCCAGCTGGATATACCCCATCATATGAATTAACGAGACTTACACCTGATGGCCAAAGCG	1577
QY	1448	AGTATGGGAAGATATAGAAACAGATTTTGTGCTCACTTATGGGCTGGGCTGGAATTGACG	1507
Db	1578	AGTATGGGAAGATATAGAGACAGATCTCCGCTCACTTATATGGGCGGCTGAGATGCACT	1637
QY	1508	ATGTGCAAAACCCAAATTATCTCGATGTAAATTATGAAGATTATGAACCTGCACGCAATG	1567
Db	1638	ACGAGACAAACCCAAATTATCCCTGAAGTCTCTATGAAGACT---GGACCAACGCCAACTG	1694
QY	1568	ACATTCGGGGAACACACGAGCAAGAAAGTATGAAATCCCTTCCACAGACCTCATCTATAAA	1627
Db	1695	ACATTGGGGGAATATCTAGCAACAAAGTATGAAATCCCTTCCACAGATTTGCTACCAA	1754
QY	1628	CCGGTCGGGAACATCTCTCGGCTATATGCTGTGATGGTATGGTGGCGTGTGGGGAATTT	1687
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QY	1688	GCCTTTGGTATATGCTGTTTCTGCTTAAGTTGGCAAGCACTCCAAAGTTTGGCATGAAG	1747
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QY	1748	GCCCAAGCTCCGCTTATACGCAATGA	1772
Db	1875	GAGGAAGCGGCTGATTTATGATGA	1899

RESULT 4	
AC009606	
LOCUS	AK009606 1832 bp mRNA linear HTC 03-APR-2004
DEFINITION	Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310034C05 product:CDJ245M18.1 (PLACENTAL PROTEIN DIFF40) [FRAGMENT] homolog [Homo sapiens], full insect sequence.
ACCESSION	AK009606
VERSION	AK009606.1 GI:128444502
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Euteleostomi; Eutelestomii Eutelestomii; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomii; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 Carninci,P. and Hayashizaki,Y. High-efficiency long-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 99279253
JOURNAL MEDLINE	2 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) 20499374
PUBMED	11042159
REFERENCE	3
AUTHORS	Kono,H., Itoh,M., Aizawa,K., Nagacka,S., Sasaki,N., Carninci,P., Shimada,A., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A., Yanamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiyagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Onara,E., Watanabe,M., Takeda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multichannel sequencer Genome Res. 10 (11), 1757-1771 (2000)
JOURNAL MEDLINE	20530913
PUBMED	11076861
REFERENCE	4
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection

JOURNAL
REFERENCE
AUTHORS

TITLE

JOURNAL
REFERENCE
AUTHORS

Nature 409, 685-690 (2001)

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1832)

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukushima, Y., Furuno, M., Hanagaki, T., Harada, A., Hayashida, N., Himeno, K., Hitachi, T., Horii, F., Imoroi, K., Ineli, Y., Itoh, M., Izawa, M., Kanekawa, T., Katoh, H., Kawaji, J., Kohjima, Y., Komori, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Niimi, K., Nomura, K., Numasaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Salto, R., Salto, R., Sakai, C., Sakai, K., Sano, H., Saeki, D., Shibata, K., Shibata, Y., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Terajima, Y., Toyota, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

Direct Submission
Submitted (10-JULY-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

Please visit our web site (<http://genome.gsc.riken.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5'-GAGAGAAGACAGATCCAGAGCTCTTTTTCCTTTTTTYN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'-GAAGAGAGATTCTCAGTAATTAATAAATATGCCCCCCCCC 3']. cDNA was cleaved with XhoI and SclI. Cloning sites, 5' end: XhoI, 3' end: SclI.

Host: SOBR.

Location/Qualifiers

1..1832

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/issue_type="tongue"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev_stage="adult"

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/note="D245M18.1 (PLACENTAL PROTEIN DIFF40) (FRAGMENT) homolog [Homo sapiens] (SPR109U124, evidence: FASTV, 97.6%ID, 100%length, match=252)"

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Best Local Similarity 80.9%; Pred. No. 8.9e-213;
Matches 1151; Conservative 0; Mismatches 248; Indels 23; Gaps 10;

ORIGIN

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Db 9 CTGACTGGCACTGGCAGCTCGGATGTGCTCTGCTGGAAGTGCATGGACCCGCCATGG 68

Gy 389 CGGGCTCTGGGGCTTTCGCTGCTGATGTGGCTTCTGGAGGGCCGCTTGGCTGTC 448

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Gy 449 CCAGGCTCGGAATGAGTGCCTCTCGGATCTGATGTCAGAGCAACCTTCTCTCGCATCG 508


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Qy      1048 GGTAACTGCTTTCCAAACATATGATGAAACAAAGCCACACAGAGGCTCTTAAAGATA 1107
Db      265 GGTAACTGCTTTCCAAACATATGATGAAACAAAGCCACACAGAGGCTCTTAAAGATA 206
Qy      1108 ACTAACTTTGATCGATGACAGTGGGAAGACATCTTGTGTGGCGGAATCTTGTGA 1167
Db      205 ACTAACTTTGATCGATGACAGTGGGAAGACATCTTGTGTGGCGGAATCTTGTGA 146
Qy      1168 GGAAGAGTCAAGATTTCTGCAACTCTGTCGATTTTGGACCAACTATCAATTTCTC 1227
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Qy      1228 GAATCTCCAACTTCAACCACTGCTGTCATCTTCATTTCACTGTGAAAAGCACTCCCAA 1287
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Qy      1288 CCAAGCGCTTCAAGTGTCTATTAAG 1312
Db      25 CCAAGCGCTTCAAGTGTCTATTAAG 1

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RESULT 6
LOCUS      BX452621      887 bp      mRNA      linear      EST 06-MAY-2004
DEFINITION BX452621 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
            CS0DN003YE01 5-PRIME, mRNA sequence.
ACCESSION  BX452621
VERSION     BX452621.2 GI:47065467
KEYWORDS    EST.
SOURCE      Homo sapiens (human)

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ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 887)
            Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
            Full-length cDNA libraries and normalization
            Unpublished (2001)
COMMENT     On May 22, 2003 this sequence version replaced gi:31028369.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
            was not normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
            This sequence belongs to sequence cluster 5428.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?cs=CS0BA00712A08_CS06777_2ac=5428.f

FEATURES
            source
                location/Qualifiers
                1..887
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="CS0DN003YE01"
                /issue_type="ADULT BRAIN"
                /dev_stage="adult"
                /clone_lib="Homo sapiens ADULT BRAIN"
                /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
                was primed with a NotI-oligo(dT) primer. Five prime end
                enriched, double-strand cDNA was digested with Not I and
                cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                vector. Library was not normalized."

ORIGIN
Query Match      21.2%; Score 786; DB 5; Length 887;
Best Local Similarity 96.9%; Pred. No. 4.8e-189;
Matches 812; Conservative 0; Mismatches 25; Indels 1; Gaps 1;

Qy      36 GAGAGTCCCGAGCGCGCGGTGTCGCGCGCGCGCGCGCATGACGAGCGCGCGC 95
Db      1 GAGTCCCGAGCGCGCGGTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 60
Qy      96 GCGAGCTCCGAGGAGCGGTAGCGCCGCCCTGTAAACGGTTCGCTATGCGGAGCACT 155
Db      61 GCGAGCTCCGAGGAGCGGTAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 120
Qy      156 GTGAACCTTCCGCGCTGCGGAACACTTTCGCTCCGAGCCAGCTCAAGCTTGATTAAC 215
Db      121 GTGAACCTTCCGCGCTGCGGAACACTTTCGCTCCGAGCCAGCTCAAGCTTGATTAAC 180
Qy      216 TGGACTGGGACGCGCGCGCAACAGCAACGAGATTAAAGAGCGGAAAGCGGAGGAAG 275
Db      181 TGGACTGGGACGCGCGCGCAACAGCAACGAGATTAAAGAGCGGAAAGCGGAGGAAG 240
Qy      276 GCTCCCGGACGCGGTGGGGAAGCGCGGTGTCAGCGCGGAGACAGCACTCGGCTG 335
Db      241 GCTCCCGGACGCGGTGGGGAAGCGCGGTGTCAGCGCGGAGACAGCACTCGGCTG 300
Qy      336 GCACTGCTCTAGAGATGTCGCTTGTGATTAAGTGTGACATGACCCGCGCATGCGGCT 395
Db      301 GCACTGCTCTAGAGATGTCGCTTGTGATTAAGTGTGACATGACCCGCGCATGCGGCT 360
Qy      396 CTGGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 455
Db      361 CTGGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Qy      456 CTGCAATGACAGTGCCTCTCGATCTGTGACAGCACTTCTCTGAGCATGTGGCATTT 515
Db      421 CTGCAATGACAGTGCCTCTCGATCTGTGACAGCACTTCTCTGAGCATGTGGCATTT 480

```

Qy 516 TCCGAGATTGGAGCCTTAACAGTGTAGATCTGAGAACATCCAGAAATTTTCATCGCAA 575
Db 481 TCCGAGATTGGAGCCTTAACAGTGTAGATCTGAGAACATCCAGAAATTTTCATCGCAA 540
Qy 576 CCAGAAAAGGTTAGAAAATCAACAGAGATGATCTTAAGCTTAATGTGGAGCTGAGAA 635
Db 541 CCAGAAAAGGTTAGAAAATCAACAGAGATGATCTTAAGCTTAATGTGGAGCTGAGAA 600
Qy 636 TCTGACAAATTTGATTTGATTTAAATTTTGGCTCATTAAGCATTTCTGAAAAACAG 695
Db 601 TCTGACAAATTTGATTTGATTTAAATTTTGGCTCATTAAGCATTTCTGAAAAACAG 660
Qy 696 CAACCTGACGACATCAATTTTACCCGAAACAACTGACGAGTTTGTCTAGAAAACATTT 755
Db 661 CAACCTGACGACATCAATTTTACCCGAAACAACTGACGAGTTTGTCTAGAAAACATTT 720
Qy 756 CCGTCACTTGAATCTTGTCTGAACATGATCTGTGGGCAATCATTTAATGCTCTGTGA 815
Db 721 CCGTCACTTGAATCTTGTCTGAACATGATCTGTGGGCAATCATTTAATGCTCTGTGA 780
Qy 816 CATTATGTGAAACAAGATCTTCAAGAGAGC-TAAATCCAGTCCAGACATCAGATTT 872
Db 781 CATTATGTGAAACAAGATCTTCAAGAGAGCTTAAATCCAGTCCAGACATCAGATTT 838

RESULT 7
B1832862 789 bp mRNA linear EST 04-OCT-2001
LOCUS 60308242881 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5221663 5',
DEFINITION mRNA sequence.
ACCESSION B1832862
VERSION B1832862.1 GI:15944412
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 789)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9apbds-rc@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNI at:
http://lmni1557.row.g column: 08
Plate: LMNI1557 row: g column: 08
High quality sequence scop: 788.
Location/Qualifiers
1. 789
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5221663"
/lab_host="DH10B"
/clone_id="NIH_MGC_120"
/note="Organ: pooled pancreas and spleen; Vector:
pCWV-SORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 19.3%; Score 714.6; DB 4; Length 789;
Best Local Similarity 97.6%; Pred. No. 8.1e-171;

Matches 768; Conservative 0; Mismatches 14; Indels 5; Gaps 4;
Qy 184 TTCGCTCCGAGCAGACTCAGCCTCTGATTAAGCTGGAAGCTGCGACGCCGCAACAGCAC 243
Db 1 TTCGCTCCGAGCAGACTCAGCCTCTGATTAAGCTGGAAGCTGCGACGCCGCAACAGCAC 60
Qy 244 GAGGAGTTAAGAGAGCCGCAAGCCGAGGAAAGCCTTCCCGCACCGGTGGGGGAAAGCGG 303
Db 61 GAGGAGTTAAGAGAGCCGCAAGCCGAGGAAAGCCTTCCCGCACCGGTGGGGGAAAGCGG 119
Qy 304 CCGGTGACGCGCGGGGACAGGCACTTGGGGCTGCGACTGCGATGAGGATATGCTCTCG 363
Db 120 CCGGTGACGCGCGGGGACAGGCACTTGGGGCTGCGACTGCGATGAGGATATGCTCTCG 179
Qy 364 ATAAGTGCATGTGAGACCGCATGAGCGGCTCTGCGGCTTCTGCTGAGTGTGGGC 423
Db 180 ATAAGTGCATGTGAGACCGCATGAGCGGCTCTGCGGCTTCTGCTGAGTGTGGGC 239
Qy 424 TTCTGAGGGGCGGCTTTGCGCTGTCCACGTCCTGCAATGCAAGTCCCTCGATCTGG 483
Db 240 TTCTGAGGGGCGGCTTTGCGCTGTCCACGTCCTGCAATGCAAGTCCCTCGATCTGG 299
Qy 484 TGCAGCAACCTTCTCTCTGCGCATGTGGCATTTCCGAGATTGAGACCTTAACAGTATAG 543
Db 300 TGCAGCAACCTTCTCTCTGCGCATGTGGCATTTCCGAGATTGAGACCTTAACAGTATAG 359
Qy 544 CCTGAGAACATCACCGAAATTTTCATGCGCAACCGAAGAAAGTTAGAAAT--CATCAAG 601
Db 360 CCTGAGAACATCACCGAAATTTTCATGCGCAACCGAAGAAAGTTAGAAATTCATCAACG 419
Qy 602 AAGATG-ATGTTGAAGCTTATGTGGGACTGAGAAATCTGACATTTGTGATTTCTGATTA 660
Db 420 AAGATGATGTGGAAGCTTATGTGGGACTGAGAAATCTGACATTTGTGATTTCTGATTA 479
Qy 661 AATTTTGGCTCATTAAGCATTTTCTGAAAAACGCAACCTGCGACATCATATTTTACC 720
Db 480 CAATTTGGCTCATTAAGCATTTTCTGAAAAACGCAACCTGCGACATCATATTTTACC 539
Qy 721 CGAAACAACATGAGAGGTTGTCTAGAGAAACATTTCCGTCACCTTGACTGTGAACTG 780
Db 540 CGAAACAACATGAGAGGTTGTCTAGAGAAACATTTCCGTCACCTTGACTGTGAACTG 599
Qy 781 ATCTGCTGGGCAATTCATTTACATGCTCTGTGACATTAATGTGATCAAGACTCTCCAA 840
Db 600 ATCTGCTGGGCAATTCATTTACATGCTCTGTGACATTAATGTGATCAAGACTCTCCAA 659
Qy 841 GAGGCTAAATCACTGACGACATCTGAGATTTGTACTGCTGAATGAAAGAGC-AGAA 899
Db 660 GAGGCTAAATCACTGACGACATCTGAGATTTGTACTGCTGAATGAAAGAGCAGAAAGAA 719
Qy 900 TATTCCTCTGGCAAACTGCGAGATACCAATTTGTGTGTCATCTGCAATCTGGCGCG 959
Db 720 TATTCCTCTGGCAAACTGCGAGATACCAATTTGTGTGTCATCTGCAATCTGGCGCG 779
Qy 960 ACCTAAC 966
Db 780 ACCTAAC 786

RESULT 8
CF410870 880 bp mRNA linear EST 02-SEP-2003
LOCUS CF410870
DEFINITION CH3#069_H10MF Canine heart normalized cDNA library in pbluescript
Canis familiaris cDNA clone CH3#069_H10 5', mRNA sequence.
ACCESSION CF410870
VERSION CF410870.1 GI:34412116
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedata; Canidae; Canis.
1 (bases 1 to 880)
Yi,Y., Deaai,R., Oiarie,M., Henthorn,P. and George A.L.

Query Match	18.8%	Score 695.8	DB 7	Length 880
Best Local Similarity	91.9%	Pred. No. 5.3e-166		
Matches 733	Conservative	0	Mismatches 65	Indels 0
			Gaps	0
Db	442	GCCTGTCCACGCTCTCTGCAAAATGACAGTCCCTCTCGAATCTGGTGACGACCCCTTCTCT	501	
Qy	83	GCCTGTCCACGCTCTCTGCAAAATGACAGTCCCTCTCGAATCTGGTGACGACCCCTTCTCT	142	
Db	502	GGCATCTGGGCAATTTCCGAGATTTGGAGCCTTAACAGTGAATCTCTGAGAACATCCGAA	561	
Qy	143	GGCATCTGGGCAATTTCCGAGATTTGGAGCCTTAACAGTGAATCTCTGAGAACATCCGAA	202	
Db	562	ATTTTCATCGCAAAACGAGAAAGTTGAAATCATCAAGAAAGATGTTGAAGCTAT	621	
Qy	203	ATTTTCATCGCAAAACGAGAAAGTTGAAATCATCAAGAAAGATGTTGAAGCTAT	262	
Db	622	GTGGAGCTGAGAAATCTGACATTTGTGATTTCTGATTTAAATTTGTGGCTCATTAAGCA	681	
Qy	263	GTGGAGCTGAGAAATCTGACATTTGTGATTTCTGATTTAAATTTGTGGCTCATTAAGCA	322	
Db	662	TTTCTGAAAAACAGCAACCTGACGACATCAATTTTACCCGAAACAACTGACAGTTG	741	
Qy	333	TTTCTGAAAAACAGCAACCTGACGACATCAATTTTACCCGAAACAACTGACAGTTG	382	
Db	742	TCTAGGAAACATTTCCGTCACCTTGAATCTTGTCTGAATCTCTGTGGGCAATTCATTT	801	
Qy	383	TCTAGGAAACATTTCCGTCACCTTGAATCTTGTCTGAATCTCTGTGGGCAATTCATTT	442	
Db	802	ACATGCTCTGTGACATTAATGATGATCAAGACTCTTCAAGAGGCTTAATTCAGTCCAGAC	861	
Qy	443	ACATGCTCTGTGACATTAATGATGATCAAGACTCTTCAAGAGGCTTAATTCAGTCCAGAC	502	
Db	862	ACTGAGATTTGTACTGCTGATGATGAAAGCAGACAGAAATATTCCTGTGGCAACCTGAC	921	
Qy	503	ACTGAGATTTGTACTGCTGATGATGAAAGCAGACAGAAATATTCCTGTGGCAACCTGAC	562	
Db	922	ATACCAATTTGTGTTTGGCATCTGCAATCTGGCCGACCTTAACCTCACTGTGGAGAA	981	
Qy	563	ATACCAATTTGTGTTTGGCATCTGCAATCTGGCCGACCTTAACCTCACTGTGGAGAA	622	

Qy	982	GGAAAGCTATCATCTATTCCTGTAGTGTGGCAGAGTGATCCGGTTCTTAATATGTATTGG	1041
Db	623	GGAAAGCTATCATCTATTCCTGTAGTGTGGCAGAGTGATCCGGTTCTTAATATGTATTGG	682
Qy	1042	GATGTGGTATCCGTGTTTCCAAATATGTAATGAACCAAGCCACACAGAGGCTCTCTTA	1101
Db	663	GATGTGGTATTCGTGTTTCCAAATATGTAATGAACCAAGCCACACAGAGGCTCTCTTG	742
Qy	1102	AGGATTAACCTAATTCATTCCTGATGACAGTGGGAGGAGATCTTGTGTGGCGAAAT	1161
Db	743	AGGATTAACCTAATTCATTCCTGATGACAGTGGGAGGAGATCTTGTGTGGCGAAAT	802
Qy	1162	CTGTGAGGAGAAATGCAAGATTTCTGTGAACCTCACTGTGCACTTTTGACCAACATATACA	1221
Db	803	CTGTGAGGAGAAATGCAAGATTTCTGTGAACCTCACTGTGCACTTTTGCTCAACTATACCA	862
Qy	1222	TTTCTCGAATCTCCAAACC	1239
Db	863	TTTCTCGAATCTCCAAACC	880
RESULT 9			
LOCUS	AY403257	627 bp	DNA linear GSS 12-DEC-2003
DEFINITION	Homo sapiens HCM1497 gene, VIRUTAL TRANSCRIPT, partial sequence,		
ACCESSION	AY403257		
VERSION	AY403257.1		
KEYWORDS	GSS.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Bukacinski, Metacore, Chordata, Craniata, Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 627)		
TITLE	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejalrajal, A., Todd, M.A., Tenenbaum, D.M., Clivello, D.R., Lu, F., Murphy, B., Perrella, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.		
JOURNAL	Direct Submision		
PUBLISHED	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
REFERENCE	Science 302 (5652), 1960-1963 (2003)		
AUTHORS	2 (bases 1 to 627)		
TITLE	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejalrajal, A., Todd, M.A., Tenenbaum, D.M., Clivello, D.R., Lu, F., Murphy, B., Perrella, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.		
JOURNAL	Direct Submision		
PUBLISHED	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
REFERENCE	Science 302 (5652), 1960-1963 (2003)		
AUTHORS	2 (bases 1 to 627)		
TITLE	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejalrajal, A., Todd, M.A., Tenenbaum, D.M., Clivello, D.R., Lu, F., Murphy, B., Perrella, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.		
JOURNAL	Direct Submision		
PUBLISHED	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
REFERENCE	Science 302 (5652), 1960-1963 (2003)		
AUTHORS	2 (bases 1 to 627)		
TITLE	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejalrajal, A., Todd, M.A., Tenenbaum, D.M., Clivello, D.R., Lu, F., Murphy, B., Perrella, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.		
JOURNAL	Direct Submision		
PUBLISHED	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
REFERENCE	Science 302 (5652), 1960-1963 (2003)		
AUTHORS	2 (bases 1 to 627)		
TITLE	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejalrajal, A., Todd, M.A., Tenenbaum, D.M., Clivello, D.R., Lu, F., Murphy, B., Perrella, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.		
JOURNAL	Direct Submision		
PUBLISHED	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
REFERENCE	Science 302 (5652), 1960-1963 (2003)		
AUTHORS	2 (bases 1 to 627)		
TITLE	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejalrajal, A., Todd, M.A., Tenenbaum, D.M., Clivello, D.R., Lu, F., Murphy, B., Perrella, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.		
JOURNAL	Direct Submision		
PUBLISHED	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
REFERENCE	Science 302 (5652), 1960-1963 (2003)		
AUTHORS	2 (bases 1 to 627)		
TITLE	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejalrajal, A., Todd, M.A., Tenenbaum, D.M., Clivello, D.R., Lu, F., Murphy, B., Perrella, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.		
JOURNAL	Direct Submision		
PUBLISHED	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
REFERENCE	Science 302 (5652), 1960-1963 (2003)		
AUTHORS	2 (bases 1 to 627)		
TITLE	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejalrajal, A., Todd, M.A., Tenenbaum, D.M., Clivello, D.R., Lu, F., Murphy, B., Perrella, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.		
JOURNAL	Direct Submision		
PUBLISHED	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
REFERENCE	Science 302 (5652), 1960-1963 (2003)		
AUTHORS	2 (bases 1 to 627)		
TITLE	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejalrajal, A., Todd, M.A., Tenenbaum, D.M., Clivello, D.R., Lu, F., Murphy, B., Perrella, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.		
JOURNAL	Direct Submision		
PUBLISHED	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
REFERENCE	Science 302 (5652), 1960-1963 (2003)		
AUTHORS	2 (bases 1 to 627)		
TITLE	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejalrajal, A., Todd, M.A., Tenenbaum, D.M., Clivello, D.R., Lu, F., Murphy, B., Perrella, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.		
JOURNAL	Direct Submision		
PUBLISHED	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
REFERENCE	Science 302 (5652), 1960-1963 (2003)		
AUTHORS	2 (bases 1 to 627)		
TITLE	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejalrajal, A., Todd, M.A., Tenenbaum, D.M., Clivello, D.R., Lu, F., Murphy, B., Perrella, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.		
JOURNAL	Direct Submision		
PUBLISHED	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
REFERENCE	Science 302 (5652), 1960-1963 (2003)		
AUTHORS	2 (bases 1 to 627)		

QY 2314 CATATAGCCAGCAGATCGCCGCGGCGATGCTTACCTGCGCTCCAGCACTTGTCAC 2373
DB 121 CATATAGCCAGCAGATCGCCGCGGCGATGCTTACCTGCGCTCCAGCACTTGTCAC 180
QY 2374 CGCATTTGGCCACACAGAACTGCTGTCGGGGAACTTGCTGTGTAATAATGGGGAC 2433
DB 181 CGCATTTGGCCACACAGAACTGCTGTCGGGGAACTTGCTGTGTAATAATGGGGAC 240
QY 2434 TTTGGAGTGTCCGGGAGCTGTACAGCACTACTACTACAGAGTGGGGCCACCAATG 2493
DB 241 TTTGGAGTGTCCGGGAGCTGTACAGCACTACTACTACAGAGTGGGGCCACCAATG 300
QY 2494 CTGGCCATTCTGCTGATGCTTCCAGAGAGCATCTGTACAGAAATTACACGAGAAAGC 2553
DB 301 CTGGCCATTCTGCTGATGCTTCCAGAGAGCATCTGTACAGAAATTACACGAGAAAGC 360
QY 2554 GAGCTCTGAGAGCTGGGGGCTGTGTGTGGAGATTTTACCTATGCAAAACGCTGG 2613
DB 361 GAGCTCTGAGAGCTGGGGGCTGTGTGTGGAGATTTTACCTATGCAAAACGCTGG 420
QY 2614 TACAGCTGTCAAACAATGAGTGTATGATGATCTACAGAGGCGGAGTCTGCAAGCA 2673
DB 421 TACAGCTGTCAAACAATGAGTGTATGATGATCTACAGAGGCGGAGTCTGCAAGCA 480
QY 2674 CCCCAGCTGCCCCCAGAGAGTGTATGAGCTGATGCTGGGGTCTGGCAGCAGAGGCC 2733
DB 481 CCCCAGCTGCCCCCAGAGAGTGTATGAGCTGATGCTGGGGTCTGGCAGCAGAGGCC 540
QY 2734 CACATGAGAGAAACATCAAGAGGATCCATCCCTCTTCAAACTTGCCAGGCACT 2793
DB 541 CACATGAGAGAAACATCAAGAGGATCCATCCCTCTTCAAACTTGCCAGGCACT 600
QY 2794 CCGGCTTACCTGAGCATTTAGGCTAG 2820
DB 601 CCGGCTTACCTGAGCATTTAGGCTAG 627

RESULT 10
LOCUS CB521879 846 bp mRNA linear EST 09-JUL-2003
DEFINITION UI-M-GH0-ceo-k-15-0-UI.r1 NIH_BMAP_GH0 Mus musculus cDNA clone
CB521879
IMAGE:6842344 5', mRNA sequence.
ACCESSION CB521879
VERSION CB521879.1 GI:29355234
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 846)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: rgs@bbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousef1.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: pYX-5.

FEATURES
Location/Qualifiers
1..846

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6842344"
/tissue_type="whole brain"

/dev_stage="1, 5, and 15 days newborn"
/lab_host="DH10B (T1 phage resistant)"
/clone_1lb="NIH BMAP GH0"
/note="Organ: Brain; Vector: pYX-Asc; Site 1: Ecor I;
Site 2: Not I. The library was constructed according
Bonaïdo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with Ecor I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAAGTGAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN

Query Match 16.8%; Score 622.6; DB 6; Length 846;

Best Local Similarity 85.5%; Pred. No. 2.66-147;
Matches 726; Conservative 0; Mismatches 118; Indels 5; Gaps 3;

QY 857 CAGACACTCAGATTTGACTGCTGATGAAAGCAGCAGAAATATTCCTGGCAACC 916
DB 1 CCGACACTCAGATTTGACTGCTGATGAAAGCAGCAGAAATATTCCTGGCAACC 60
QY 917 TGCAGATACCCAAATTTGTTGTCATCTGCAAACTTGGCCGCACTTAACCTGTGG 976
DB 61 TGCAGATACCCAAATTTGTTGTCATCTGCAAACTTGGCCGCACTTAACCTGTGG 120
QY 977 AGGAAGGAAGTCTATCATATCTGTAATGAGAGAGTGGATCCGGTCTTAATAGT 1036
DB 121 AGGAAGGAAGTCTGTAACCTTCTGCAAGTGGGGGGTGAACCACTCCCACTTGT 180
QY 1037 ATTGGAGTGTGTAACTGTAACCTGTTTCAAAACATATGAATGAACCAACAGAGGCT 1096
DB 181 ACTGGAGCTTGGGAATTTGGTTTCAAGCAATGAAATGAACCAACAGAGGCT 240
QY 1097 CTTTAAAGATTAAGTAACTTTCAATCCAGTGAAGTGGAGCAGATCTCTTGTGGCG 1156
DB 241 CTTTAAAGATTAAGTAACTTTCAATCCAGTGAAGTGGAGCAGATCTCTTGTGGCG 300
QY 1157 AAAATCTTGAAGGAAGATTAAGTCTGCAACCTCACTGTCATTTTGCACCAACTA 1216
DB 301 AAAATCTTGAAGGAAGATTAAGTCTGCAACCTCACTGTCATTTTGCACCAACTA 360
QY 1217 TCACATTTCTGATCTCCAACTCAGACCACTGGTGATTCATTCACTGTGAAG 1276
DB 361 TCACATTTCTGATCTCCAACTCAGACCACTGGTGATTCATTCACTGTGAAG 420
QY 1277 GCAACCCCAACGACGGCTTCAAGTGTCTTAAACGCGGCAATATTGAATGATCCAAT 1336
DB 421 GCAACCCCAACGACGGCTTCAAGTGTCTTAAACGCGGCAATATTGAATGATCCAAT 480
QY 1337 ACATCTGTACTAAATACATGTTACCAATCAACAGAGTACCAAGGCTGCTCCAGCTGG 1396
DB 481 ACATCTGTACTAAATACATGTTACCAATCAACAGAGTACCAAGGCTGCTCCAGCTGG 540
QY 1397 ATATCCCACTCAGATGAACAAATGGGGACTCACTTAATGACCAAGAAATGATAGGA 1456
DB 541 ATATCCCACTCAGATGAACAAATGGGGACTCACTTAATGACCAAGAAATGATAGGA 600
QY 1457 AGATGAGAAACAGATTTGCTGCTCACTTCAATGGGCTGGATTTGACAGATGGTGA 1516
DB 601 AGATGAGAAACAGATTTGCTGCTCACTTCAATGGGCTGGATTTGACAGATGGTGA 659
QY 1517 ACCCAATATCTCTGATGATATTTATGAAGTTATGAACCTGACGCAATGACATCGGG 1576
DB 660 ACCCAATATCTCTGATGATATTTATGAAGTTATGAACCTGACGCAATGACATCGGG 716
QY 1577 ACACCAAGAACAGAAATGAATATCCCTTCAACAGAGTCACTGATTTAAACCGGTCGG 1636


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Db      717 ATATACGAACAAAGTAATGAAATCCCTCCAGGATGTTGCTGACAAAGCAATGGG 776
Qy      1637 AACATCTCTGGTCTATGCTGTGGT-GATGATTCGCTGTGTGGGATTTTGGCTTTTG 1695
Db      777 AGCATCTCTGGTCTATGCGGTGGTGTGATTCGATCTGTGGGATTTCTGCTCTG 836
Qy      1696 GATATGCTG 1704
Db      837 GTGATGTTG 845

RESULT 11
AL707530 615 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZp686f0348.r1.686 (synonym: h1cc3) Homo sapiens cDNA clone
DEFINITION DKFZp686f0348.5', mRNA sequence.
ACCESSION AL707530
VERSION AL707530.1 GI:19690885
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 615)
AUTHORS Lauber,J., Bahr,A., Mewes,H.W., Weil,B., Amid,C., Oeanger,A.,
Fobo,G., Han,M. and Wiemann,S.
EST (Lauber,J., Bahr,A., Mewes,H.W., Weil,B., Amid,C., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
LOCUS This is the 5' sequence of the clone insert
DEFINITION Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No s1 sequence available.
This clone (DKFZp686f0348) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
source
1..615
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="DKFZp686f0348"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="686 (synonym: h1cc3)"
/note="Vector: pTriplex2; Site_1: sf11A; Site_2: sf11B;
cDNA-collection"

ORIGIN
Query Match 16.5%; Score 611.8; DB 1; Length 615;
Best Local Similarity 99.7%; Pred. No. 1.4e-144;
Matches 613; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1759 GTTATGAGCAATGATGATGATCTGCGCAGCCCACTGCATCATCTCCAAATGGAGTAAC 1818
Db 1 GTTATGAGCAATGATGATGATCTGCGCAGCCCACTGCATCATCTCCAAATGGAGTAAC 60

Qy 1819 ACTTCATCTTCTTGGAGAGTGCGCCAGATCTGTCATTTATGGAATGACCAAGATCCCT 1878
Db 61 ACTTCATCTTCTTGGAGAGTGCGCCAGATCTGTCATTTATGGAATGACCAAGATCCCT 120

Qy 1879 GTCAATGAAATCCCGAGTACTTTGGCATCAACCAAGTCAGCTCAAGCCAGACATTT 1938
Db 121 GTCAATGAAATCCCGAGTACTTTGGCATCAACCAAGTCAGCTCAAGCCAGACATTT 180

Qy 1939 GTTACAGCAATCAAGCCAGATTAATGTTCTTGAAGAGGAGCTAGAGGAGAGGCTTT 1998
Db 181 GTTACAGCAATCAAGCCAGATTAATGTTCTTGAAGAGGAGCTAGAGGAGAGGCTTT 240

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Qy 1999 GAAAAAGTTTCTAGCTGATGCTATTAACCTCTGTCTGAGCAAGCAAGATCTTGGTG 2058
Db 241 GAAAAAGTTTCTAGCTGATGCTATTAACCTCTGTCTGAGCAAGCAAGATCTTGGTG 300

Qy 2059 GCAGTGAAGACCTGGAAGATGCGAGTGAACAATGACGCAAGGACTTCCACCGTAGGCC 2118
Db 301 GCAGTGAAGACCTGGAAGATGCGAGTGAACAATGACGCAAGGACTTCCACCGTAGGCC 360

Qy 2119 GAGCTCTGACCAACCTCCAGCATGAGCAGATGCTCAAGTTCTATGAGCGTGTGGAG 2178
Db 361 GAGCTCTGACCAACCTCCAGCATGAGCAGATGCTCAAGTTCTATGAGCGTGTGGAG 420

Qy 2179 GCGGACCCCTCATCATGCTCTTTTGTAGTACATGAAGATGGGACTCAAGTTCTTC 2238
Db 421 GCGGACCCCTCATCATGCTCTTTTGTAGTACATGAAGATGGGACTCAAGTTCTTC 480

Qy 2239 AGGCGACAGCGCCCTGATGCGCGTGTGATGGCTGAGGGCAACCGGCCAGAGACTAG 2298
Db 481 AGGCGACAGCGCCCTGATGCGCGTGTGATGGCTGAGGGCAACCGGCCAGAGACTAG 540

Qy 2299 CAGTCGAGATGCTGATATAGCCAGCAGATGCGCGGCGCATGTCTACCTGGCGCTCC 2358
Db 541 CAGTCGAGATGCTGATATAGCCAGCAGATGCGCGGCGCATGTCTACCTGGCGCTCC 600

Qy 2359 CAGCACTTCTGTGAC 2373
Db 601 CAGCACTTCTGTGAC 615

RESULT 12
AL603196 601 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZp686j092.r1.686 (synonym: h1cc3) Homo sapiens cDNA clone
DEFINITION DKFZp686j092.5', mRNA sequence.
ACCESSION AL603196
VERSION AL603196.1 GI:1516702
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 601)
AUTHORS Wambutt,R., Heubner,D., Mewes,H.W., Weil,B. and Wiemann,S.
TITLE EST (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B. and Wiemann,S.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
LOCUS This is the 5' sequence of the clone insert
DEFINITION Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No s1 sequence available.
This clone (DKFZp686j092) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
source
1..601
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686j092"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="686 (synonym: h1cc3)"
/note="Vector: pTriplex2; Site_1: sf11A; Site_2: sf11B;
cDNA-collection"

ORIGIN
Query Match 16.2%; Score 601; DB 1; Length 601;
Best Local Similarity 100.0%; Pred. No. 7.9e-142;

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Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 642 AATTGGATTCGTGATTAATAATTTGGCTCAATAAGCATTTCTGAAAAAGCAACT 701
 Db 1 AATTGGATTCGTGATTAATAATTTGGCTCAATAAGCATTTCTGAAAAAGCAACT 60

QY 702 GCAGCAGATCAATTTTACCCGAAACAAACTGACGAGTTTCTGAGAAACATTTCCGTCA 761
 Db 61 GCAGCAGATCAATTTTACCCGAAACAAACTGACGAGTTTCTGAGAAACATTTCCGTCA 120

QY 762 CCTTGACTTGTCTGAACTGATCCCTGGTGGCAATCCATTTTCAATGCTCCCTGACATTA 821
 Db 121 CCTTGACTTGTCTGAACTGATCCCTGGTGGCAATCCATTTTCAATGCTCCCTGACATTA 180

QY 822 GTGATCAAGACTCTCCAGAGGCTTAATCAAGTCCAGACACTGAGATTGTACTGCT 881
 Db 181 GTGATCAAGACTCTCCAGAGGCTTAATCAAGTCCAGACACTGAGATTGTACTGCT 240

QY 882 GAATGAAGAGCAAGAAATATTCCTGCGAAACCTGACAGATACCAATTGTGTTGCC 941
 Db 241 GAATGAAGAGCAAGAAATATTCCTGCGAAACCTGACAGATACCAATTGTGTTGCC 300

QY 942 ATCTGCAATCTGCGCCGACCTTAACCTCACTGTGAGAGAAAGAAAGTCTATCAATTATC 1001
 Db 301 ATCTGCAATCTGCGCCGACCTTAACCTCACTGTGAGAGAAAGAAAGTCTATCAATTATC 360

QY 1002 CTGTAGTGTGGAGGTATCCGTTCTTAATATGTAATGAGATGTGTAACCTGTTTC 1061
 Db 361 CTGTAGTGTGGAGGTATCCGTTCTTAATATGTAATGAGATGTGTAACCTGTTTC 420

QY 1062 CAACATATGATGAATGAACCAAGCAGACAGAGGCTCTTAAGATACTAATTTATC 1121
 Db 421 CAACATATGATGAATGAACCAAGCAGACAGAGGCTCTTAAGATACTAATTTATC 480

QY 1122 CGATGACAGTGGAGAGAGATCTTGTGTGGCGAAATCTTTAGAGAGATCAAGA 1181
 Db 481 CGATGACAGTGGAGAGAGATCTTGTGTGGCGAAATCTTTAGAGAGATCAAGA 540

QY 1182 TTCTGTCAACTGCTGTGATTTTGAACCAATATCAATTTTCAATCTCAATCTC 1241
 Db 541 TTCTGTCAACTGCTGTGATTTTGAACCAATATCAATTTTCAATCTCAATCTC 600

QY 1242 A 1242
 Db 601 A 601

RESULT 13
 BP434087 893 bp mRNA linear EST 30-DEC-2003
 LOCUS BP434087 full-length enriched swine cDNA library, adult lung Sus
 DEFINITION scrofa cDNA clone LMG010047B02 5', mRNA sequence.
 ACCESSION BP434087
 VERSION BP434087.1 GI:40424154
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 1 (bases 1 to 893)
 Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
 Okumura,N., Hamashima,N. and Awata,T.
 PEDS (Pig EST Data Explorer): construction of a database for ESTs
 derived from porcine full-length cDNA libraries
 Nucleic Acids Res. 32 (1), D484-D488 (2004)
 Contact: Hirohide Uenishi
 Animal Genome Laboratory, Genome Research Department
 National Institute of Agricultural Sciences
 2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
 Tel: +81-29-838-8627
 Fax: +81-29-838-8627
 Email: huenishi@affrc.go.jp
 EST project with full-length enriched cDNA libraries carried out in

Animal Genome Research Program (Japan) by National Institute of
 Agricultural Sciences and STAFF-Institute
 Single pass sequencing of clones derived from oligo-capped cDNA
 library
 Vector sequences were eliminated by RepeatMasker version 2002/07/13
 and crossmatch version 0.990319
 Low quality bases were trimmed based on the quality values.

FEATURES

source
 1. .893
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 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /clone="LMG010047B02"
 /tissue_type="lung"
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 lung"

ORIGIN

Query Match 16.2%; Score 600.4; DB 5; Length 893;
 Best Local Similarity 93.8%; Pred. No. 1.2e-141;
 Matches 625; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 1083 CCAACACAGGCTCTCTTAAGATTAATTAATTTCAATCCGATGACAGTGGAGCAAT 1142
 Db 1 CCAACACAGGCTCTCTTAAGATTAATTAATTTCAATCCGATGACAGTGGAGCAAT 60

QY 1143 CTCTGTGTGGCGGAAATCTGTAGAGAGATCAAGATTTCTGTCAACTCACTGATCA 1202
 Db 61 CTCTGTGTGGCGGAAATCTGTAGAGAGATCAAGATTTCTGTCAACTCACTGATCA 120

QY 1203 TTTTGGACCAACTATCAATTTCTGATCTCAATCTCAAGCTCAGACCACTGATGCTCC 1262
 Db 121 TTTTGGCTCAACTATCAATTTCTGATCTCAATCTCAAGCTCAGACCACTGATGCTCC 180

QY 1263 ATTCACTGTGAAGCAACCCCAACAGGCTTCACTGTTCTATTAAGGGGCAATTT 1322
 Db 181 ATTCACTGTGAAGCAACCCCAACAGGCTTCACTGTTCTATTAAGGGGCAATTT 240

QY 1323 GAATGAGTCCAAATATCACTGTACTAATAATCAATGTTACCAATCAACGAGTACCAAG 1382
 Db 241 GAATGAGTCCAAATATCACTGTACTAATAATCAATGTTACCAATCAACGAGTACCAAG 300

QY 1383 CTGCTTCAGCTGATATATCTTACTCATGAAACATGGGACTCAAGTTAGTGGCTCA 1442
 Db 301 CTGCTTCAGCTGATATATCTTACTCATGAAACATGGGACTCAAGTTAGTGGCTCA 360

QY 1443 GAATGAGTATGGAGAGATGAGAAACAGATTTCTGCTCACTTCATGAGGCTGCTGAT 1502
 Db 361 GAATGAGTATGGAGAGATGAGAAACAGATTTCTGCTCACTTCATGAGGCTGCTGAT 420

QY 1503 TGACGATGTGCAAAACCAATTAATCTGATGTAATTAATTAATGAATATGCAATGCAAC 1562
 Db 421 TGACGATGTGCAAAACCAATTAATCTGATGTAATTAATTAATGAATATGCAATGCAAC 480

QY 1563 GAATGACATGGGAGCAACCAAGAAAGATTAATTAATTAATTAATTAATTAATTAATTA 1622
 Db 481 GAATGACATGGGAGCAACCAAGAAAGATTAATTAATTAATTAATTAATTAATTAATTA 540

QY 1623 TAAACCGTTCGGGACATCTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 1682
 Db 541 TAAACCGTTCGGGACATCTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 600

QY 1683 ATTTGCTTTTGTGTAATGCTGTTTCTGCTTAAGTGGCAAGACATTCGAATTTGGCAT 1742
 Db 601 ATTTGCTTTTGTGTAATGCTGTTTCTGCTTAAGTGGCAAGACATTCGAATTTGGCAT 660

QY 1743 GAAAGG 1748
 Db 661 GAAAGG 666

RESULT 14

BP250017
LOCUS BP250017 587 bp mRNA linear EST 15-SEP-2004
DEFINITION BP250017 Sugano cDNA library, hippocampus Homo sapiens cDNA clone
HPR01277, mRNA sequence.
ACCESSION BP250017
VERSION BP250017
KEYWORDS BP250017.1 GI:52132296
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 587)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
JOURNAL Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
COMMENT Location/Qualifiers
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/clone="HPR01277"
/issue_type="hippocampus"
/clone_lib="Sugano cDNA library, hippocampus"
ORIGIN
Query Match 15.8%; Score 585; DB 5; Length 587;
Best Local Similarity 100.0%; Pred. No. 9.6e-138;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
461 AATGCAATGCTCTCCGATCTGTCGACGACCCCTTCTCCGCGATGTCGACATTTCCGA 520
Db 1 AATGCAATGCTCTCCGATCTGTCGACGACCCCTTCTCCGCGATGTCGACATTTCCGA 60
Qy 521 GATTGAGCCTTAACAGTGTAGATCCTGAGAACATCACCGAAATTTTCATGCAACAGCA 580
Db 61 GATTGAGCCTTAACAGTGTAGATCCTGAGAACATCACCGAAATTTTCATGCAACAGCA 120
Qy 581 AAAGTTAGAAATCATCAACGAAAGATGTTGAAGCTTATGTCGACCTGAGAAATCTGA 640
Db 121 AAAGTTAGAAATCATCAACGAAAGATGTTGAAGCTTATGTCGACCTGAGAAATCTGA 180
Qy 641 CAATTGAGATCTGAGATTAATAATTTGGGCTCATAAAGCATTTCTGAAAAACGCAACC 700
Db 181 CAATTGAGATCTGAGATTAATAATTTGGGCTCATAAAGCATTTCTGAAAAACGCAACC 240
Qy 701 TGCAGCATCAATTTTACCAGAAACAACTGACGAGTTTGTCTAGGAAACATTTCCGTC 760
Db 241 TGCAGCATCAATTTTACCAGAAACAACTGACGAGTTTGTCTAGGAAACATTTCCGTC 300
Qy 761 ACCTTGACTGTCTGAACCTGATCCTGTCGTCGCAATTCATTAACCTGCTGTCACATTA 820
Db 301 ACCTTGACTGTCTGAACCTGATCCTGTCGTCGCAATTCATTAACCTGCTGTCACATTA 360
Qy 821 TGTGATCAAGACTCTCCAGAGGCTAAATCCAGTCCAGACACTCGAGATTGTAATGCC 880
Db 361 TGTGATCAAGACTCTCCAGAGGCTAAATCCAGTCCAGACACTCGAGATTGTAATGCC 420
Qy 881 TGAATGAAGCAAGAAATATTCCTCCGTCGCAACCTGTCAGATCCCAATTTGGTGGC 940
Db 421 TGAATGAAGCAAGAAATATTCCTCCGTCGCAACCTGTCAGATCCCAATTTGGTGGC 480
Qy 941 CATCTGCAAAATCTGCGCGACCTTAACCTCACTGTGAGAGAAAGTCTATCAATTAT 1000
Db 481 CATCTGCAAAATCTGCGCGACCTTAACCTCACTGTGAGAGAAAGTCTATCAATTAT 540
Qy 1001 CCGTAGTGTGGCAGGTGATCCGGTTCCTAATATGATTTGGGATG 1045

Db 541 CCGTAGTGTGGCAGGTGATCCGGTTCCTAATATGATTTGGGATG 585
|||||
RESULT 15
BP439194
LOCUS BP439194 881 bp mRNA linear EST 30-DEC-2003
DEFINITION BP439194 full-length enriched swine cDNA library, adult lung Sue
scrofa cDNA clone UMG010102603 5', mRNA sequence.
ACCESSION BP439194
VERSION BP439194
KEYWORDS BP439194.1 GI:40429261
SOURCE EST.
ORGANISM Sus scrofa (pig)
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 881)
Uenishi, H., Egnuchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H.,
Okumura, N., Hamashima, N. and Awata, T.
PBDE (Pig EST Data Explorer): construction of a database for ESTs
derived from porcine full-length cDNA libraries
Nucleic Acids Res. 32 (1), D484-D488 (2004)
JOURNAL Contact: Hirohide Uenishi
Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Fax: +81-29-838-8627
Email: huenishi@affrc.go.jp
EST project with full-length enriched cDNA libraries carried out in
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
library
Vector sequences were eliminated by RepeatMasker version 2002/07/13
and crossmatch version 0.990319
Low quality bases were trimmed based on the quality values.
FEATURES
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lung"
ORIGIN
Query Match 15.8%; Score 585; DB 5; Length 881;
Best Local Similarity 93.8%; Pred. No. 1.1e-137;
Matches 609; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
Qy 1100 TAAGATTAATCAATTTCAATCCAGTACAGTGGAGAGCAGATCTCTTGTCGCGGAAA 1159
Db 2 TAAGATTAATCAATTTCAATCCAGTACAGTGGAGAGCAATCTCTGTGTGCAAGAAA 61
Qy 1160 ATCTTGAGAGAGATCAAGATCTGTCAACCTCACTGTGATTTGGACCAACTATCA 1219
Db 62 ATCTTGAGAGAGATCAAGATCTGTCAACCTCACTGTGATTTGGCTGCAACTATCA 121
Qy 1220 CATTTCTGAATCTCAACCTCAAGACCACTGTGTGATTCATTCATCTGTGAAGGCA 1279
Db 122 CATTTCTGAATCTCAACCTCAAGACCACTGTGTGATTCATTCATCTGTGAAGGCA 181
Qy 1280 ACCCCAAACGAGGCTTCAGTGGTTCTTATAACGGGGCAATTTGAATGAATCCAAATACA 1339
Db 182 ACCCCAAACGAGGCTTCAGTGGTTCTTATAACGGGGCAATTTGAATGAATCCAAATACA 241
Qy 1340 TCTGTACTAAATATCATGTTACCAATCACACGAGATCACACGAGCTGCTCCAGCTGATA 1399
Db 242 TCTGTACTAAATATCATGTTACCAATCACACGAGATCACACGAGCTGCTCCAGCTGATA 301

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